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(57) Abstract

The present invention relates to the field of glycosylation engineering of proteins. More particularly, the present invention is directed to the glycosylation engineering of proteins to provide proteins with improved therapeutic properties, e.g., antibodies, antibody fragments, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin, with enhanced Fc–mediated cellular cytotoxicity.

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GLYCOSYLATION ENGINEERING OF ANTIBODIES FOR IMPROVING ANTIBODY-DEPENDENT CELLULAR CYTOTOXICITY

I. RELATION TO OTHER APPLICATIONS

This application claims priority to United States Provisional Application Serial No. 60/082,581, filed April 20, 1998, incorporated herein by reference in its entirety.

II. FIELD OF THE INVENTION

The present invention relates to the field of glycosylation engineering of proteins. More particularly, the present invention relates to glycosylation engineering to generate proteins with improved therapeutic properties, including antibodies with enhanced antibody-dependent cellular cytotoxicity.

III. BACKGROUND OF THE INVENTION

Glycoproteins mediate many essential functions in human beings, other eukaryotic organisms, and some prokaryotes, including catalysis, signalling, cell-cell communication, and molecular recognition and association. They make up the majority of non-cytosolic proteins in eukaryotic organisms. Lis and Sharon, 1993, *Eur. J. Biochem.* 218:1-27. Many glycoproteins have been exploited for therapeutic purposes, and during the last two decades, recombinant versions of naturally-occurring, secreted glycoproteins have been a major product of the biotechnology industry. Examples include erythropoietin (EPO), therapeutic monoclonal antibodies (therapeutic mAbs), tissue plasminogen activator (tPA), interferon-β, (IFN-β), granulocyte-macrophage colony stimulating factor (GM-CSF), and human chorionic gonadotrophin (hCH). Cumming *et al.*, 1991, *Glycobiology* 1:115-130.

The oligosaccharide component can significantly affect properties relevant to the efficacy of a therapeutic glycoprotein, including physical stability, resistance to protease attack, interactions with the immune system, pharmacokinetics, and specific biological activity. Such properties may depend not only on the presence or absence, but also on the specific structures, of oligosaccharides. Some generalizations between oligosaccharide structure and glycoprotein function can be made. For example, certain oligosaccharide structures mediate rapid clearance of the glycoprotein from the

bloodstream through interactions with specific carbohydrate binding proteins, while others can be bound by antibodies and trigger undesired immune reactions. Jenkins *et al.*, 1996, *Nature Biotechn.* 14:975-981.

Mammalian cells are the preferred hosts for production of therapeutic glycoproteins, due to their capability to glycosylate proteins in the most compatible form for human application. Cumming, 1991, *supra*; Jenkins *et al.*, 1996, *supra*. Bacteria very rarely glycosylate proteins, and like other types of common hosts, such as yeasts, filamentous fungi, insect and plant cells, yield glycosylation patterns associated with rapid clearance from the blood stream, undesirable immune interactions, and in some specific cases, reduced biological activity. Among mammalian cells, Chinese hamster ovary (CHO) cells have been most commonly used during the last two decades. In addition to giving suitable glycosylation patterns, these cells allow consistent generation of genetically stable, highly productive clonal cell lines. They can be cultured to high densities in simple bioreactors using serum-free media, and permit the development of safe and reproducible bioprocesses. Other commonly used animal cells include baby hamster kidney (BHK) cells, NS0- and SP2/0-mouse myeloma cells. More recently, production from transgenic animals has also been tested. Jenkins *et al.*, 1996, *supra*.

The glycosylation of recombinant therapeutic proteins produced in animal cells can be engineered by overexpression of glycosyl transferase genes in host cells. Bailey, 1991, *Science* 252:1668-1675. However, previous work in this field has only used constitutive expression of the glycoprotein-modifying glycosyl transferase genes, and little attention has been paid to the expression level.

IV. SUMMARY OF THE INVENTION

The present invention is directed, generally, to host cells and methods for the generation of proteins having an altered glycosylation pattern resulting in improved therapeutic values. In one specific embodiment, the invention is directed to host cells that have been engineered such that they are capable of expressing a preferred range of a glycoprotein-modifying glycosyl transferase activity which increases complex N-linked oligosaccharides carrying bisecting GlcNAc. In other embodiments, the present invention is directed to methods for the generation of modified glycoforms of glycoproteins, for example antibodies, including whole antibody molecules, antibody

fragments, or fusion proteins that include a region equivalent to the Fc region of an immunoglobulin, having an enhanced Fc-mediated cellular cytotoxicity, and glycoproteins so generated. The invention is based, in part, on the inventors' discovery that there is an optimal range of glycoprotein-modifying glycosyl transferase expression for the maximization of complex N-linked oligosaccharides carrying bisecting GlcNAc.

More specifically, the present invention is directed to a method for producing altered glycoforms of proteins having improved therapeutic values, *e.g.*, an antibody which has an enhanced antibody dependent cellular cytotoxicity (ADCC), in a host cell. The invention provides host cells which harbor a nucleic acid encoding the protein of interest, *e.g.*, an antibody, and at least one nucleic acid encoding a glycoprotein-modifying glycosyl transferase. Further, the present invention provides methods and protocols of culturing such host cells under conditions which permit the expression of said protein of interest, *e.g.*, the antibody having enhanced antibody dependent cellular cytotoxicity. Further, methods for isolating the so generated protein having an altered glycosylation pattern, *e.g.*, the antibody with enhanced antibody dependent cellular cytotoxicity, are described.

Furthermore, the present invention provides alternative glycoforms of proteins having improved therapeutic properties. The proteins of the invention include antibodies with an enhanced antibody-dependent cellular cytotoxicity (ADCC), which have been generated using the disclosed methods and host cells.

V. BRIEF DESCRIPTION OF THE DRAWINGS

FIGURE 1 depicts the representation of typical Fc-associated oligosaccharide structures.

FIGURE 2 depicts a Western blot analysis of tetracycline-regulated expression of GnT III in two different tTA-producing CHO clones. CHOt2 (lanes A and B) and CHOt17 (lanes C and D) cells were transfected with the pUDH10-3GnTIIIm expression vector and cultured for 36 h in the absence (lanes A and C) or presence of tetracycline, at a concentration of 400 ng/ml (lanes B and D). Cell lysates were then prepared for western blot analysis probing with an antibody (9E10), which recognizes specifically the c-myc tag added to GnT III at its carboxy-terminus.

FIGURE 3 depicts determination of the range of tetracycline concentrations where myc-tagged GnT III expression can be controlled. CHOt17 cells were transfected

with the pUDH10-3-GnTIIIm expression vector and then cultured for 48h in the presence of the indicated concentrations of tetracycline. GnT III levels in cell lysates from these cultures were compared using western blot analysis. GnT III was detected *via* the c-myc tag using 9E10 antibody.

FIGURES 4A through 4B depict screening of CHO clones for stable, tetracycline-regulated expression of GnT V (FIGURE 4A) or myc-tagged GnT III (FIGURE 4B) glycosyltransferases by western blot analysis. CHOt17 cells were co-transfected with a vector for expression of puromycin resistance (pPUR) and either pUHD10-3GnTV (FIGURE 4A) or pUDH10-3GnTIIIm (FIGURE 4B) and stable CHO clones were selected for resistance to puromycin (7.5 μ/ml), in the presence of tetracycline (2 μg/ml). Eight clones (1-8) for each glycosyltransferase were cultured for 48 h in the absence or presence (+) of tetracycline (2 μg/ml) and analysed by western blot using either an anti-GnT V antibody (FIGURE 4A) or an anti-myc (9E10) antibody (FIGURE 4B).

FIGURES 5A and 5B depict verification of activity of heterologous GnT V (FIGURE 5A) and Gn T III (FIGURE 5B) glycosyltransferaseas *in vivo* by lectin blot analysis. Cellular glycoproteins from various stable clones (numbered as in FIGURE 4), cultured in the absence or presence (+) of tetracycline (2 μg/ml), were resolved by SDS-PAGE, blotted to a membrane, and probed with either L-PHA (FIGURE 5A) or E-PHA (FIGURE 5B) lectins. These lectins bind with higher affinity to the oligosaccharide products of reactions catalyzed by GnT V and GnT III, respectively, than to the oligosaccharide substrates of these reactions. A molecular weight marker (MWM) was run in parallel. A comparison of lectin blots in FIGURES 5A and 5B indicates a broader range of substrates, among the endogenous CHO cell glycoproteins, for GnT III (FIGURE 5B) than for GnT V (FIGURE 5A).

FIGURES 6A through 6D depict inhibition of cell growth upon glycosyltransferase overexpression. CHO-tet-GnTIIIm cells were seeded to 5-10% confluency and cultured in the absence (FIGURES 6A and 6B) or presence (FIGURES 6C and 6D) of tetracycline. Cultures were photographed 45 (FIGURES 6A and 6C) and 85 (FIGURES 16B and 6D) hours after seeding.

FIGURE 7 depicts sequences of oligonucleotide primers used in PCRs for the construction of the chCE7 heavy chain gene. Forward and reverse primers are identified by the suffixes ".fwd" and ".rev", respectively. Overlaps between different

primers, necessary to carry out secondary PCR steps using the product of a primary PCR step as a template, are indicated. Restriction sites introduced, sequences annealing to the CE7 chimeric genomic DNA, and the synthetic leader sequence introduced, are also indicated.

FIGURE 8 depicts sequences of oligonucleotide primers used in PCRs for the construction of the chCE7 light chain gene. Forward and reverse primers are identified by the suffixes ".fwd" and ".rev" respectively. Overlaps between different primers, necessary to carry out secondary PCR steps using as a template the product of a primary PCR step, are indicated. Restriction sites introduced, sequences annealing to the CE7 chimeric genomic DNA, and the leader sequence introduced, are also indicated.

FIGURE 9 depicts MALDI/TOF-MS spectra of neutral oligosaccharide mixtures from chCE7 samples produced either by SP2/0 mouse myeloma cells (FIGURE 9A, oligosaccharides from 50 μg of CE7-SP2/0), or by CHO-tetGnTIII-chCE7 cell cultures differing in the concentration of tetracycline added to the media, and therefore expressing the GnT III gene at different levels. In decreasing order of tetracycline concentration, *i.e.*, increasing levels of GnT III gene expression, the latter samples are: CE7-2000t (FIGURE 9B, oligosaccharides from 37.5μg of antibody), CE7-60t (FIGURE 9C, oligosaccharides from 37.5 μg of antibody, CE7-30t (FIGURE 9D, oligosaccharides from 25 μg of antibody) and CE7-15t (FIGURE 9E, oligosaccharides from 10 μg of antibody).

FIGURE 10 depicts N-linked oligosaccharide biosynthetic pathways leading to bisected complex oligosaccharides *via* a GnT III-catalyzed reaction. M stands for Mannose; Gn, N-acetylglucosamine (GlcNAc); G, galactose; Gn^b, bisecting GlcNAc; f, fucose. The oligosaccharide nomenclature consists of enumerating the M, Gn, and G residues attached to the core oligosaccharide and indicating the presence of a bisecting GlcNAc by including a Gn^b. The oligosaccharide core is itself composed of 2 Gn residues and may or may not include a fucose. The major classes of oligosaccharides are shown inside dotted frames. Man I stands for Golgi mannosidase; GnT, GlcNAc transferase; and GalT, for galactosyltransferase. The mass associated with the major, sodium-associated oligosaccharide ion that is observed MALDI/TOF-MS analysis is shown beside each oligosaccharide. For oligosaccharides which can potentially be core-fucosylated, the masses associated with both fucosylated (+f) and non-fucosylated (-f) forms are shown.

FIGURE 11 depicts N-linked oligosaccharide biosynthetic pathway leading to bisected complex and bisected hybrid oligosaccharides *via* GnT III-catalyzed reactions. M stands for mannose; Gn N-acetylglucosamine (GlcNAc); G, galactose; Gn^b, bisecting GlcNAc; f, fucose. The oligosaccharide nomenclature consists of enumerating the M, Gn, and G residues attached to the common oligosaccharide and indicating the presence of bisecting GlcNAc by including a Gn^b. The oligosaccharide core is itself composed of 2 Gn residues and may or not include a fucose. The major classes of oligosaccharides are shown inside dotted frames. Man I stands for Golgi mannosidase; TnT, GlcNAc transferase; and GalT, for galactosyltransferase. The mass associated with major, sodium-associated oligosaccharide ion that is observed in MALDI/TOF-MS analysis is shown beside each oligosaccharide. For oligosaccharides which can potentially be core-fucosylated, the masses associated with both fucosylated (+f) and non -fucosylated (-f) forms are shown.

FIGURE 12 depicts ADCC activity of different chCE7 samples. Lysis of IMR-32 neuroblastoma cells by human lymphocytes (target:effector ratio of 1:19, 16 h incubation at 37 °C), mediated by different concentrations of chCE7 samples, was measured *via* retention of a fluorescent dye. The percentage of cytotoxicity is calculated relative to a total lysis control (by means of a detergent), after subtraction of the signal in the absence of antibody.

FIGURE 13 depicts the GnT III expression of different cultures of CHO-tet-GnTIII grown at different tetracycline concentrations used to produce distinct C2B8 antibody samples. Cell lysates from each culture grown at 2000ng/ml (Lane C) and 25ng/ml (Lane D) tetracycline concentrations were resolved by SDS-PAGE, blotted onto a membrane, and probed with 9E10 (*see supra)* and anti-mouse horseradish peroxidase as primary and secondary antibodies, respectively. Lane A depicts a negative control.

FIGURES 14A and 14B depict the specificity of antigen binding of the C2B8 anti-CD20 monoclonal antibody using an indirect immunofluorescence assay with cells in suspension. CD20 positive cells (SB cells; ATCC deposit no.ATCC CCL120) and CD20 negative cells (HSB cells; ATCC deposit no. ATCC CCL120.1), FIGURE 14A and 14B respectively, were utilized. Cells of each type were incubated with C2B8 antibody produced at 25ng/ml tetracycline as a primary antibody. Negative controls included HBSSB instead of primary antibody. An anti-human IgG Fc specific,

polyclonal, FITC conjugated antibody was used for all samples as a secondary antibody.

FIGURE 15 depicts the ADCC activity of different C2B8 antibody samples at different antibody concentrations (0.04-5μg/ml). Sample C2B8-nt represents the ADCC activity of the C2B8 antibody produced in a cell line without GnT III expression. Samples C2B8-2000t, C2B8-50t and C2B8-25t show the ADCC activity of three antibody samples produced at decreasing tetracycline concentrations (i.e., increasing GnT III expression).

VI. DEFINITIONS

Terms are used herein as generally used in the art, unless otherwise defined in the following:

As used herein, the term ***antibody*** is intended to include whole antibody molecules, antibody fragments, or fusion proteins that include a region equivalent to the Fc region of an immunoglobulin.

As used herein, the term ***glycoprotein-modifying glycosyl transferase*** refers to an enzyme that effects modification of the glycosylation pattern of a glycoprotein. Examples of glycoprotein-modifying glycosyl transferases include, but are not limited to glycosyl transferases such as GnT III, GnT V, GalT, and Man II.

As used herein, the term ***glycosylation engineering*** is considered to include any sort of change to the glycosylation pattern of a naturally occurring polypeptide or fragment thereof. Glycosylation engineering includes metabolic engineering of the glycosylation machinery of a cell, including genetic manipulations of the oligosaccharide synthesis pathways to achieve altered glycosylation of glycoproteins expressed in cells. Furthermore, glycosylation engineering includes the effects of mutations and cell environment on glycosylation.

As used herein, the term ***host cell*** covers any kind of cellular system which can be engineered to generate modified glycoforms of proteins, protein fragments, or peptides of interest, including antibodies and antibody fragments. Typically, the host cells have been manipulated to express optimized levels of at least one glycoprotein-modifying glycosyl transferase, including, but not limited to GnT III, GnT V, GalT, and Man II, and/or at least one glycosidase. Host cells include cultured cells, *e.g.*, mammalian cultured cells, such as CHO cells, BHK cells, NS0 cells, SP2/0 cells, or hybridoma cells, yeast cells, and insect cells, to name only few, but also cells comprised

within a transgenic animal or cultured tissue.

As used herein, the term ***Fc-mediated cellular cytotoxicity*** is intended to include antibody dependent cellular cytotoxicity (ADCC), and cellular cytotoxicity directed to those cells that have been engineered to express on their cell surface an Fc-region or equivalent region of an immunoglobin G, and cellular cytotoxicity mediated by a soluble fusion protein consisting of a target protein domain fused to the N-terminus of an Fc-region or equivalent region of an immunoglobulin G.

VII. DETAILED DESCRIPTION OF THE INVENTION

A. General Overview

The objective of the present invention is to provide glycoforms of proteins, in particular antibodies, including whole antibody molecules, antibody fragments, or fusion proteins that include a region equivalent to the Fc region of an immunoglobulin, to produce new variants of a therapeutic protein. The invention is based, in part, on the inventors' discovery that the glycosylation reaction network of a cell can be manipulated to maximize the proportion of certain glycoforms within the population, and that certain glycoforms have improved therapeutic characteristics. The invention is further based, in part, on the discovery of ways to identify glycoforms of proteins which have an improved therapeutic value, and how to generate them reproducibly. The invention is further based, in part, on the discovery that there is a preferred range of glycoprotein-modifying glycosyl transferase expression in the antibody-generating cell, for increasing complex N-linked oligosaccharides carrying bisecting GlcNAc.

As such, the present invention is directed, generally, to methods for the glycosylation engineering of proteins to alter and improve their therapeutic properties. More specifically, the present invention describes methods for producing in a host cell an antibody which has an altered glycosylation pattern resulting in an enhanced antibody dependent cellular cytotoxicity (ADCC). For the practice of the methods, the present invention provides host cells which harbor a nucleic acid encoding an antibody and at least one nucleic acid encoding a glycoprotein-modifying glycosyl transferase. Further, the present invention provides methods and protocols of culturing such host cells under conditions which permit the expression of the desired antibody having an altered glycosylation pattern resulting in an enhanced antibody dependent cellular

cytotoxicity. Further, methods for isolating the so generated antibody with enhanced antibody dependent cellular cytotoxicity are described.

In more specific embodiments of the invention, two monoclonal antibodies, namely the anti-neuroblastoma antibody chCE7, and the anti-CD20 antibody C2B8, have been used as model therapeutic glycoproteins, and the target glycoforms have been those carrying a special class of carbohydrate, namely bi-antennary complex N-linked oligosaccharides modified with bisecting N-acetylglucosamine (GlcNAc). In the model system provided by the invention, CHO cells are used as host cells, although many other cell systems may be contemplated as host cell system. The glycosyl transferase that adds a bisecting GlcNAc to various types of N-linked oligosaccharides, GlcNAc-transferase III (GnT III), is not normally produced by CHO cells. Stanley and Campell, 1984. *J. Biol. Chem.* 261:13370-13378.

To investigate the effects of GnT III overexpression experimentally, a CHO cell line with tetracycline-regulated overexpression of a rat GnT III cDNA was established. Using this experimental system, the inventors discovered that overexpression of GnT III to high levels led to growth inhibition and was toxic to the cells. Another CHO cell line with tetracycline-regulated overexpression of GnT V, which is a distinct glycosyl transferase, showed the same inhibitory effect, indicating that this may be a general feature of glycoprotein-modifying glycosyl transferase overexpression. The effect of the enzyme expression on the cell growth sets an upper limit to the level of glycoprotein-modifying glycosyl transferase overexpression and may therefore also limit the extent to which poorly accessible glycosylation sites can be modified by engineering of glycosylation pathways and patterns using unregulated expression vectors.

The production of a set of chCE7 mAb and C2B8 samples differing in their glycoform distributions by controlling GnT III expression in a range between basal and toxic levels are disclosed. Measurement of the ADCC activity of the chCE7 mAb samples showed an optimal range of GnT III expression for maximal chCE7 *in vitro* biological activity. The activity correlated with the level of Fc-associated bisected, complex oligosaccharides. Expression of GnT III within the practical range, *i.e.*, where no significant growth inhibition and toxicity are observed, led to an increase of the target bisected, complex structures for this set of chCE7 samples. The pattern of oligosaccharide peaks in MALDI/TOF-mass spectrometric analysis of chCE7 samples

produced at high levels of GnT III indicates that a significant proportion of potential GnT III substrates is diverted to bisected hybrid oligosaccharide by-products. Minimization of these by-products by further engineering of the pathway could therefore be valuable.

B. Identification And Generation Of Nucleic Acids Encoding A Protein For Which Modification Of The Glycosylation Pattern Is Desired

The present invention provides host cell systems suitable for the generation of altered glycoforms of any protein, protein fragment or peptide of interest, for which such an alteration in the glycosylation pattern is desired. The nucleic acids encoding such protein, protein fragment or peptide of interest may be obtained by methods generally known in the art. For example, the nucleic acid may be isolated from a cDNA library or genomic library. For a review of cloning strategies which may be used, *see*, *e.g.*, Maniatis, 1989, Molecular Cloning, A Laboratory Manual, Cold Springs Harbor Press, N.Y.; and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, (Green Publishing Associates and Wiley Interscience, N.Y.).

In an alternate embodiment of the invention, the coding sequence of the protein, protein fragment or peptide of interest may be synthesized in whole or in part, using chemical methods well known in the art. *See*, for example, Caruthers *et al.*, 1980, *Nuc. Acids Res. Symp. Ser.* 7:215-233; Crea and Horn, 1980, *Nuc. Acids Res. USA* 9:2331; Matteucci and Caruthers, 1980, *Tetrahedron Letters* 21:719; Chow and Kempe, 1981, *Nuc. Acids Res.* 9:2807-2817. Alternatively, the protein itself could be produced using chemical methods to synthesize its amino acid sequence in whole or in part. For example, peptides can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography. *E.g.*, *see* Creighton, 1983, Protein Structures And Molecular Principles, W.H. Freeman and Co., N.Y. pp. 50-60. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; *see* Creighton, 1983, Proteins, Structures and Molecular Principles, W.H. Freeman and Co., N.Y., pp. 34-49).

In preferred embodiments, the invention provides methods for the generation and use of host cell systems for the production of glycoforms of antibodies or antibody

fragments or fusion proteins which include antibody fragments with enhanced antibody-dependent cellular cytotoxicity. Identification of target epitopes and generation of antibodies having potential therapeutic value, for which modification of the glycosylation pattern is desired, and isolation of their respective coding nucleic acid sequence is within the scope of the invention.

Various procedures known in the art may be used for the production of antibodies to target epitopes of interest. Such antibodies include but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments and fragments produced by an Fab expression library. Such antibodies may be useful, *e.g.*, as diagnostic or therapeutic agents. As therapeutic agents, neutralizing antibodies, *i.e.*, those which compete for binding with a ligand, substrate or adapter molecule, are of especially preferred interest.

For the production of antibodies, various host animals are immunized by injection with the target protein of interest including, but not limited to, rabbits, mice, rats, etc. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Monoclonal antibodies to the target of interest may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B-cell hybridoma technique (Kosbor *et al.*, 1983, *Immunology Today* 4:72; Cote *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:2026-2030) and the EBV-hybridoma technique (Cole *et al.*, 1985, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). In addition, techniques developed for the production of "chimeric antibodies" (Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci. U.S.A.* 81:6851-6855; Neuberger *et al.*, 1984, *Nature* 312:604-608; Takeda *et al.*, 1985, *Nature* 314:452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. Alternatively, techniques described for the production of single chain antibodies (U.S.

Patent No. 4,946,778) can be adapted to produce single chain antibodies having a desired specificity.

Antibody fragments which contain specific binding sites of the target protein of interest may be generated by known techniques. For example, such fragments include, but are not limited to, $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed (Huse *et al.*, 1989, *Science* 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity to the target protein of interest.

Once an antibody or antibody fragment has been identified for which modification in the glycosylation pattern are desired, the coding nucleic acid sequence is identified and isolated using techniques well known in the art. *See, supra.*

C. Generation Of Cell Lines For The Production Of Proteins With Altered Glycosylation Pattern

The present invention provides host cell expression systems for the generation of proteins having modified glycosylation patterns. In particular, the present invention provides host cell systems for the generation of glycoforms of proteins having an improved therapeutic value. Therefore, the invention provides host cell expression systems selected or engineered to increase the expression of a glycoprotein-modifying glycosyltransferase. Specifically, such host cell expression systems may be engineered to comprise a recombinant nucleic acid molecule encoding a glycoprotein-modifying glycosyltransferase, operatively linked to a constitutive or regulated promoter system. Alternatively, host cell expression systems may be employed that naturally produce, are induced to produce, and/or are selected to produce a glycoprotein-modifying glycosyltransferase.

In one specific embodiment, the present invention provides a host cell that has been engineered to express at least one nucleic acid encoding a glycoprotein-modifying glycosyl transferase. In one aspect, the host cell is transformed or transfected with a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase. In an alternate aspect, the host cell has been engineered and/or selected in such way that an endogenous glycoprotein-

modifying glycosyl transferase is activated. For example, the host cell may be selected to carry a mutation triggering expression of an endogenous glycoprotein-modifying glycosyl transferase. This aspect is exemplified in one specific embodiment, where the host cell is a CHO lec10 mutant. Alternatively, the host cell may be engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated. In again another alternative, the host cell is engineered such that an endogenous glycoprotein-modifying glycosyl transferase has been activated by insertion of a regulated promoter element into the host cell chromosome. In a further alternative, the host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase.has been activated by insertion of a constitutive promoter element, a transposon, or a retroviral element into the host cell chromosome.

Generally, any type of cultured cell line can be used as a background to engineer the host cell lines of the present invention. In a preferred embodiment. CHO cells, BHK cells, NS0 cells, SP2/0 cells, or a hybridoma cell line is used as the background cell line to generate the engineered host cells of the invention.

The invention is contemplated to encompass engineered host cells expressing any type of glycoprotein-modifying glycosyl transferase as defined herein. However, in preferred embodiments, at least one glycoprotein-modifying glycosyl transferase expressed by the host cells of the invention is GnT III, or, alternatively, ß(1,4)-N-acetylglucosaminyltransferase V (GnT V). However, also other types of glycoprotein-modifying glycosyl transferase may be expressed in the host system, typically in addition to GnT III or GnT V, including β(1,4)-galactosyl transferase (GalT), and mannosidase II (Man II). In one embodiment of the invention, GnT III is coexpressed with GalT. In another embodiment of the invention, GnT III is coexpressed with Man II. In a further embodiment of the invention, GnT III is coexpressed with GalT and Man II. However, any other permutation of glycoprotein-modifying glycosyl transferases is within the scope of the invention. Further, expression of a glycosidase in the host cell system may be desired.

One or several nucleic acids encoding a glycoprotein-modifying glycosyl transferase may be expressed under the control of a constitutive promoter or, alternately, a regulated expression system. Suitable regulated expression systems include, but are not limited to, a tetracycline-regulated expression system, an ecdysone-inducible expression system, a lac-switch expression system, a glucocorticoid-inducible

expression system, a temperature-inducible promoter system, and a metallothionein metal-inducible expression system. If several different nucleic acids encoding glycoprotein-modifying glycosyl transferases are comprised within the host cell system, some of them may be expressed under the control of a constitutive promoter, while others are expressed under the control of a regulated promoter. The optimal expression levels will be different for each protein of interest, and will be determined using routine experimentation. Expression levels are determined by methods generally known in the art, including Western blot analysis using a glycosyl transferase specific antibody, Northern blot analysis using a glycosyl transferase specific nucleic acid probe, or measurement of enzymatic activity. Alternatively, a lectin may be employed which binds to biosynthetic products of the glycosyl transferase, for example, E_4-PHA lectin. In a further alternative, the nucleic acid may be operatively linked to a reporter gene; the expression levels of the glycoprotein-modifying glycosyl transferase are determined by measuring a signal correlated with the expression level of the reporter gene. The reporter gene may transcribed together with the nucleic acid(s) encoding said glycoprotein-modifying glycosyl transferase as a single mRNA molecule; their respective coding sequences may be linked either by an internal ribosome entry site (IRES) or by a cap-independent translation enhancer (CITE). The reporter gene may be translated together with at least one nucleic acid encoding said glycoprotein-modifying glycosyl transferase such that a single polypeptide chain is formed. The nucleic acid encoding the glycoprotein-modifying glycosyl transferase may be operatively linked to the reporter gene under the control of a single promoter, such that the nucleic acid encoding the glycoprotein-modifying glycosyl transferase and the reporter gene are transcribed into an RNA molecule which is alternatively spliced into two separate messenger RNA (mRNA) molecules; one of the resulting mRNAs is translated into said reporter protein, and the other is translated into said glycoprotein-modifying glycosyl transferase.

If several different nucleic acids encoding a glycoprotein-modifying glycosyl transferase are expressed, they may be arranged in such way that they are transcribed as one or as several mRNA molecules. If they are transcribed as a single mRNA molecule, their respective coding sequences may be linked either by an internal ribosome entry site (IRES) or by a cap-independent translation enhancer (CITE). They may be transcribed from a single promoter into an RNA molecule which is alternatively spliced

into several separate messenger RNA (mRNA) molecules, which then are each translated into their respective encoded glycoprotein-modifying glycosyl transferase.

In other embodiments, the present invention provides host cell expression systems for the generation of therapeutic proteins, for example antibodies, having an enhanced antibody-dependent cellular cytotoxicity, and cells which display the IgG Fc region on the surface to promote Fc-mediated cytotoxicity. Generally, the host cell expression systems have been engineered and/or selected to express nucleic acids encoding the protein for which the production of altered glycoforms is desired, along with at least one nucleic acid encoding a glycoprotein-modifying glycosyl transferase. In one embodiment, the host cell system is transfected with at least one gene encoding a glycoprotein-modifying glycosyl transferase. Typically, the transfected cells are selected to identify and isolate clones that stably express the glycoprotein-modifying glycosyl transferase. In another embodiment, the host cell has been selected for expression of endogenous glycosyl transferase. For example, cells may be selected carrying mutations which trigger expression of otherwise silent glycoprotein-modifying glycosyl transferases. For example, CHO cells are known to carry a silent GnT III gene that is active in certain mutants, *e.g.*, in the mutant Lec10. Furthermore, methods known in the art may be used to activate silent glycoprotein-modifying glycosyl transferase genes, including the insertion of a regulated or constitutive promoter, the use of transposons, retroviral elements, etc. Also the use of gene knockout technologies or the use of ribozyme methods may be used to tailor the host cell's glycosyl transferase and/or glycosidase expression levels, and is therefore within the scope of the invention.

Any type of cultured cell line can be used as background to engineer the host cell lines of the present invention. In a preferred embodiment, CHO cells, BHK cells, NS0 cells, SP2/0 cells. Typically, such cell lines are engineered to further comprise at least one transfected nucleic acid encoding a whole antibody molecule, an antibody fragment, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin. In an alternative embodiment, a hybridoma cell line expressing a particular antibody of interest is used as background cell line to generate the engineered host cells of the invention.

Typically, at least one nucleic acid in the host cell system encodes GnT III, or, alternatively, GnT V. However, also other types of glycoprotein-modifying glycosyl transferase may be expressed in the host system, typically in addition to GnT III or GnT

V, including GalT, and Man II. In one embodimentof the invention, GnT III is coexpressed with GalT. In another embodiment of the invention, GnT III is coexpressed with Man II. In a further embodiment of the invention, GnT III is coexpressed with GalT and Man II. However, any other permutation of glycoprotein-modifying glycosyl transferases is within the scope of the invention. Further, expression of a glycosidase in the host cell system may be desired.

One or several nucleic acids encoding a glycoprotein-modifying glycosyl transferase may be expressed under the control of a constitutive promoter, or alternately, a regulated expression system. Suitable regulated expression systems include, but are not limited to, a tetracycline-regulated expression system, an ecdysone-inducible expression system, a lac-switch expression system, a glucocorticoid-inducible expression system, a temperature-inducible promoter system, and a metallothionein metal-inducible expression system. If several different nucleic acids encoding glycoprotein-modifying glycosyl transferases are comprised within the host cell system, some of them may be expressed under the control of a constitutive promoter, while others are expressed under the control of a regulated promoter. The optimal expression levels will be different for each protein of interest, and will be determined using routine experimentation. Expression levels are determined by methods generally known in the art, including Western blot analysis using a glycosyl transferase specific antibody, Northern blot analysis using a glycosyl transferase specific nucleic acid probe, or measurement of enzymatic activity. Alternatively, a lectin may be employed which binds to biosynthetic products of glycosyl transferase, for example, E_4-PHA lectin. In a further alternative, the nucleic acid may be operatively linked to a reporter gene; the expression levels of the glycoprotein-modifying glycosyl transferase are determined by measuring a signal correlated with the expression level of the reporter gene. The reporter gene may transcribed together with the nucleic acid(s) encoding said glycoprotein-modifying glycosyl transferase as a single mRNA molecule; their respective coding sequences may be linked either by an internal ribosome entry site (IRES) or by a cap-independent translation enhancer (CITE). The reporter gene may be translated together with at least one nucleic acid encoding said glycoprotein-modifying glycosyl transferase such that a single polypeptide chain is formed. The nucleic acid encoding the glycoprotein-modifying glycosyl transferase may be operatively linked to the reporter gene under the control of a single promoter, such that the nucleic acid

encoding the glycoprotein-modifying glycosyl transferase and the reporter gene are transcribed into an RNA molecule which is alternatively spliced into two separate messenger RNA (mRNA) molecules; one of the resulting mRNAs is translated into said reporter protein, and the other is translated into said glycoprotein-modifying glycosyl transferase.

If several different nucleic acids encoding a glycoprotein-modifying glycosyl transferase are expressed, they may be arranged in such way that they are transcribed as one or as several mRNA molecules. If they are transcribed as single mRNA molecule, their respective coding sequences may be linked either by an internal ribosome entry site (IRES) or by a cap-independent translation enhancer (CITE). They may be transcribed from a single promoter into an RNA molecule which is alternatively spliced into several separate messenger RNA (mRNA) molecules, which then are each translated into their respective encoded glycoprotein-modifying glycosyl transferase.

1. Expression Systems

Methods which are well known to those skilled in the art can be used to construct expression vectors containing the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. *See*, for example, the techniques described in Maniatis *et al.*, 1989, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y. and Ausubel *et al.*, 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y.

A variety of host-expression vector systems may be utilized to express the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase. Preferably, mammalian cells are used as host cell systems transfected with recombinant plasmid DNA or cosmid DNA expression vectors containing the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase. Most preferably, CHO cells, BHK cells, NS0 cells, or SP2/0 cells, or alternatively, hybridoma cells are used as host cell systems. In alternate embodiments, other eukaryotic host cell systems may be contemplated, including, yeast cells transformed with recombinant yeast expression vectors containing

the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.*, Ti plasmid) containing the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase; or animal cell systems infected with recombinant virus expression vectors (*e.g.*, adenovirus, vaccinia virus) including cell lines engineered to contain multiple copies of the DNA encoding the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase either stably amplified (CHO/dhfr) or unstably amplified in double-minute chromosomes (*e.g.*, murine cell lines).

For the methods of this invention, stable expression is generally preferred to transient expression because it typically achieves more reproducible results and also is more amenable to large scale production. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with the respective coding nucleic acids controlled by appropriate expression control elements (*e.g.*, promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows selection of cells which have stably integrated the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines.

A number of selection systems may be used, including, but not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, 1977, *Cell* 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, *Proc. Natl. Acad. Sci. USA* 48:2026), and adenine phosphoribosyltransferase (Lowy *et al.*, 1980, *Cell* 22:817) genes, which can be employed in tk^-, $hgprt^-$ or $aprt^-$ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler *et al.*, 1980, *Natl. Acad. Sci. USA*

77:3567; O'Hare *et al.*, 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, *Proc. Natl. Acad. Sci. USA* 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin *et al.*, 1981, *J. Mol. Biol.* 150:1); and hygro, which confers resistance to hygromycin (Santerre *et al.*, 1984, *Gene* 30:147) genes. Recently, additional selectable genes have been described, namely trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, 1988, *Proc. Natl. Acad. Sci. USA* 85:8047); the glutamine synthase system; and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue, 1987, *in*: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.).

2. Identification Of Transfectants Or Transformants That Express The Protein Having A Modified Glycosylation Pattern

The host cells which contain the coding sequence and which express the biologically active gene products may be identified by at least four general approaches; (a) DNA-DNA or DNA-RNA hybridization; (b) the presence or absence of "marker" gene functions; (c) assessing the level of transcription as measured by the expression of the respective mRNA transcripts in the host cell; and (d) detection of the gene product as measured by immunoassay or by its biological activity.

In the first approach, the presence of the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase(s) inserted in the expression vector can be detected by DNA-DNA or DNA-RNA hybridization using probes comprising nucleotide sequences that are homologous to the respective coding sequences, respectively, or portions or derivatives thereof.

In the second approach, the recombinant expression vector/host system can be identified and selected based upon the presence or absence of certain "marker" gene functions (*e.g.*, thymidine kinase activity, resistance to antibiotics, resistance to methotrexate, transformation phenotype, occlusion body formation in baculovirus, etc.). For example, if the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase are inserted within a marker gene sequence of the vector, recombinants containing the respective coding sequences can be

identified by the absence of the marker gene function. Alternatively, a marker gene can be placed in tandem with the coding sequences under the control of the same or different promoter used to control the expression of the coding sequences. Expression of the marker in response to induction or selection indicates expression of the coding sequence of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase.

In the third approach, transcriptional activity for the coding region of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase can be assessed by hybridization assays. For example, RNA can be isolated and analyzed by Northern blot using a probe homologous to the coding sequences of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase or particular portions thereof. Alternatively, total nucleic acids of the host cell may be extracted and assayed for hybridization to such probes.

In the fourth approach, the expression of the protein products of the protein of interest and the coding sequence of the glycoprotein-modifying glycosyl transferase can be assessed immunologically, for example by Western blots, immunoassays such as radioimmuno-precipitation, enzyme-linked immunoassays and the like. The ultimate test of the success of the expression system, however, involves the detection of the biologically active gene products.

D. Generation And Use Of Proteins And Protein Fragments Having Altered Glycosylation Patterns

1. Generation And Use Of Antibodies Having Enhanced Antibody-Dependent Cellular Cytotoxicity

In preferred embodiments, the present invention provides glycoforms of antibodies and antibody fragments having an enhanced antibody-dependent cellular cytotoxicity.

Clinical trials of unconjugated monoclonal antibodies (mAbs) for the treatment of some types of cancer have recently yielded encouraging results. Dillman, 1997, *Cancer Biother. & Radiopharm.* 12:223-225; Deo *et al.*, 1997, *Immunology Today* 18:127. A chimeric, unconjugated IgG1 has been approved for low-grade or follicular B-cell non-Hodgkin's lymphoma (Dillman, 1997, *supra*), while another unconjugated mAb, a humanized IgG1 targeting solid breast tumors, has also been

showing promising results in phase III clinical trials. Deo *et al.*, 1997, *supra*. The antigens of these two mAbs are highly expressed in their respective tumor cells and the antibodies mediate potent tumor destruction by effector cells *in vitro* and *in vivo*. In contrast, many other unconjugated mAbs with fine tumor specificities cannot trigger effector functions of sufficient potency to be clinically useful. Frost *et al.*, 1997, *Cancer* 80:317-333; Surfus *et al.*, 1996, *J. Immunother.* 19:184-191. For some of these weaker mAbs, adjunct cytokine therapy is currently being tested. Addition of cytokines can stimulate antibody-dependent cellular cytotoxicity (ADCC) by increasing the activity and number of circulating lymphocytes. Frost *et al.*, 1997, *supra*; Surfus *et al.*, 1996, *supra*. ADCC, a lytic attack on antibody-targeted cells, is triggered upon binding of lymphocyte receptors to the constant region (Fc) of antibodies. Deo *et al.*, 1997, *supra*.

A different, but complementary, approach to increase ADCC activity of unconjugated IgG1s would be to engineer the Fc region of the antibody to increase its affinity for the lymphocyte receptors (FcγRs). Protein engineering studies have shown that FcγRs interact with the lower hinge region of the IgG CH2 domain. Lund *et al.*, 1996, *J. Immunol.* 157:4963-4969. However, FcγR binding also requires the presence of oligosaccharides covalently attached at the conserved Asn 297 in the CH2 region. Lund *et al.*, 1996, *supra*; Wright and Morrison, 1997, *Tibtech* 15:26-31, suggesting that either oligosaccharide and polypeptide both directly contribute to the interaction site or that the oligosaccharide is required to maintain an active CH2 polypeptide conformation. Modification of the oligosaccharide structure can therefore be explored as a means to increase the affinity of the interaction.

An IgG molecule carries two N-linked oligosaccharides in its Fc region, one on each heavy chain. As any glycoprotein, an antibody is produced as a population of glycoforms which share the same polypeptide backbone but have different oligosaccharides attached to the glycosylation sites. The oligosaccharides normally found in the Fc region of serum IgG are of complex bi-antennary type (Wormald *et al.*, 1997, *Biochemistry* 36:130-1380), with low level of terminal sialic acid and bisecting N-acetylglucosamine (GlcNAc), and a variable degree of terminal galactosylation and core fucosylation (FIGURE 1). Some studies suggest that the minimal carbohydrate structure required for FcγR binding lies within the oligosaccharide core. Lund *et al.*, 1996, *supra*. The removal of terminal galactoses results in approximately a two-fold

reduction in ADCC activity, indicating a role for these residues in FcγR receptor binding. Lund *et al.*, 1996, *supra*.

The mouse- or hamster-derived cell lines used in industry and academia for production of unconjugated therapeutic mAbs normally attach the required oligosaccharide determinants to Fc sites. IgGs expressed in these cell lines lack, however, the bisecting GlcNAc found in low amounts in serum IgGs. Lifely *et al.*, 1995, *Glycobiology* 318:813-822. In contrast, it was recently observed that a rat myeloma-produced, humanized IgG1 (CAMPATH-1H) carried a bisecting GlcNAc in some of its glycoforms. Lifely *et al.*, 1995, *supra*. The rat cell-derived antibody reached a similar *in vitro* ADCC activity as CAMPATH-1H antibodies produced in standard cell lines, but at significantly lower antibody concentrations.

The CAMPATH antigen is normally present at high levels on lymphoma cells. and this chimeric mAb has high ADCC activity in the absence of a bisecting GlcNAc. Lifely *et al.*, 1995, *supra*. Even though in the study of Lifely *et al.*, 1995, *supra*. the maximal *in vitro* ADCC activity was not increased by altering the glycosylation pattern, the fact that this level of activity was obtained at relatively low antibody concentrations for the antibody carrying bisected oligosaccharides suggests an important role for bisected oligosaccharides. An approach was developed to increase the ADCC activity of IgG1s with low basal activity levels by producing glycoforms of these antibodies carrying bisected oligosaccharides in the Fc region.

In the N-linked glycosylation pathway, a bisecting GlcNAc is added by the enzyme β(1,4)-N-acetylglucosaminyltransferase III (GnT III). Schachter, 1986, *Biochem. Cell Biol.* 64:163-181. Lifely *et al.*, 1995, *supra*, obtained different glycosylation patterns of the same antibody by producing the antibody in different cell lines with different but non-engineered glycosylation machineries, including a rat myeloma cell line that expressed GnT III at an endogenous, constant level. In contrast, we used a single antibody-producing CHO cell line, that was previously engineered to express, in an externally-regulated fashion, different levels of a cloned GnT III gene. This approach allowed us to establish for the first time a rigorous correlation between expression of GnT III and the ADCC activity of the modified antibody.

As demonstrated herein, *see*, Example 4, *infra*, C2B8 antibody modified according to the disclosed method had an about sixteen-fold higher ADCC activity than the standard, unmodified C2B8 antibody produced under identical cell culture and

purification conditions. Briefly, a C2B8 antibody sample expressed in CHO-tTA-C2B8 cells that do not have GnT III expression showed a cytotoxic activity of about 31% (at 1μg/ml antibody concentration), measured as *in vitro* lysis of SB cells (CD20+) by human lymphocytes. In contrast, C2B8 antibody derived from a CHO cell culture expressing GnT III at a basal, largely repressed level showed at 1μg/ml antibody concentration a 33% increase in ADCC activity against the control at the same antibody concentration. Moreover, increasing the expression of GnT III produced a large increase of almost 80% in the maximal ADCC activity (at 1μg/ml antibody concentration) compared to the control at the same antibody concentration. *See*, Example 4, *infra*.

Further antibodies of the invention having an enhanced antibody-dependent cellular cytotoxicity include, but are not limited to, anti-human neuroblastoma monoclonal antibody (chCE7) produced by the methods of the invention, a chimeric anti-human renal cell carcinoma monoclonal antibody (ch-G250) produced by the methods of the invention, a humanized anti-HER2 monoclonal antibody produced by the methods of the invention, a chimeric anti-human colon, lung, and breast carcinoma monoclonal antibody (ING-1) produced by the methods of the invention, a humanized anti-human 17-1A antigen monoclonal antibody (3622W94) produced by the methods of the invention, a humanized anti-human colorectal tumor antibody (A33) produced by the methods of the invention, an anti-human melanoma antibody (R24) directed against GD3 ganglioside produced by the methods of the invention, and a chimeric anti-human squamous-cell carcinoma monoclonal antibody (SF-25) produced by the methods of the invention. In addition, the invention is directed to antibody fragment and fusion proteins comprising a region that is equivalent to the Fc region of immunoglobulins. *See, infra.*

2. Generation And Use Fusion Proteins Comprising A Region Equivalent To An Fc Region Of An Immunoglobulin That Promote Fc-Mediated Cytotoxicity

As discussed above, the present invention relates to a method for enhancing the ADCC activity of therapeutic antibodies. This is achieved by engineering the glycosylation pattern of the Fc region of such antibodies, in particular by maximizing the proportion of antibody molecules carrying bisected complex oligosaccharides N-linked to the conserved glycosylation sites in their Fc regions. This

strategy can be applied to enhance Fc-mediated cellular cytotoxicity against undesirable cells mediated by any molecule carrying a region that is an equivalent to the Fc region of an immunoglobulin, not only by therapeutic antibodies, since the changes introduced by the engineering of glycosylation affect only the Fc region and therefore its interactions with the Fc receptors on the surface of effector cells involved in the ADCC mechanism. Fc-containing molecules to which the presently disclosed methods can be applied include, but are not limited to, (a) soluble fusion proteins made of a targeting protein domain fused to the N-terminus of an Fc-region (Chamov and Ashkenazi, 1996, *TIBTECH* 14: 52) and (b) plasma membrane-anchored fusion proteins made of a type II transmembrane domain that localizes to the plasma membrane fused to the N-terminus of an Fc region (Stabila, P.F., 1998, *Nature Biotech.* 16: 1357).

In the case of soluble fusion proteins (a) the targeting domain directs binding of the fusion protein to undesirable cells such as cancer cells, *i.e.*, in an analogous fashion to therapeutic antibodies. The application of presently disclosed method to enhance the Fc-mediated cellular cytotoxic activity mediated by these molecules would therefore be identical to the method applied to therapeutic antibodies. *See*, Example 2 of United States Provisional Application Serial Number 60/082,581, incorporated herein by reference.

In the case of membrane-anchored fusion proteins (b) the undesirable cells in the body have to express the gene encoding the fusion protein. This can be achieved either by gene therapy approaches, *i.e.*, by transfecting the cells *in vivo* with a plasmid or viral vector that directs expression of the fusion protein-encoding gene to undesirable cells, or by implantation in the body of cells genetically engineered to express the fusion protein on their surface. The later cells would normally be implanted in the body inside a polymer capsule (encapsulated cell therapy) where they cannot be destroyed by an Fc-mediated cellular cytotoxicity mechanism. However should the capsule device fail and the escaping cells become undesirable, then they can be eliminated by Fc-mediated cellular cytotoxicity. Stabila *et al.*, 1998, *Nature Biotech.* 16: 1357. In this case, the presently disclosed method would be applied either by incorporating into the gene therapy vector an additional gene expression cassette directing adequate or optimal expression levels of GnT III or by engineering the cells to be implanted to express adequate or optimal levels of GnT III. In both cases, the aim of the disclosed method is to increase or maximize the proportion of surface-displayed Fc regions carrying

bisected complex oligosaccharides.

The examples below explain the invention in more detail. The following preparations and examples are given to enable those skilled in the art to more clearly understand and to practice the present invention. The present invention, however, is not limited in scope by the exemplified embodiments, which are intended as illustrations of single aspects of the invention only, and methods which are functionally equivalent are within the scope of the invention. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

VIII. EXAMPLES

A. Example 1: Tetracycline-Regulated Overexpression Of Glycosyl Transferases In Chinese Hamster Ovary Cells

To establish a cell line in which the expression of GnT III could be externally-controlled, a tetracycline-regulated expression system was used. Gossen, M. and Bujard, H., 1992, *Proc. Nat. Acad. Sci.* USA, 89: 5547-5551. The amount of GnT III in these cells could be controlled simply by manipulating the concentration of tetracycline in the culture medium. Using this system, it was found that overexpression of GnT III to high levels led to growth inhibition and was toxic to the cells. Another CHO cell line with tetracycline-regulated overexpression of GnT V, a distinct glycoprotein-modifying glycosyl transferase, showed the same inhibitory effect, indicating that this may be a general feature of glycoprotein-modifying glycosyl transferase overexpression. This phenomenon has not been reported previously, probably due to the fact that inventigators generally have used constitutive promoters for related experiments. The growth effect sets an upper limit to the level of glycoprotein-modifying glycosyl transferase overexpression, and may thereby also limit the maximum extent of modification of poorly accessible glycosylation sites.

1. Materials And Methods

Establishment Of CHO Cells With Tetracycline-Regulated Expression Of Glycosyltransferases. In a first step, an intermediate CHO cell line

(CHO-tTA) was first generated that constitutively expresses a tetracycline-controlled transactivator (tTA) at a level for the adequate for the regulation system. Using Lipofectamine reagent (Gibco, Eggenfelden, Germany), CHO (DUKX) cells were co-transfected, with *pUHD15-1*, a vector for constitutive expression of the tTA gene (Gossen and Bujard, 1992, *Proc. Nat. Acad. Sci. USA*, 89: 5547-5551), and *pSV2Neo*, a vector for constitutive expression of a neomycin resistance gene (Clontech, Palo Alto, CA). Stable, drug-resistant clones were selected and screened for adequate levels of tTA expression *via* transient transfections with a tetracycline-regulated β-galactosidase expression vector, *pUHG16-3*. C-myc epitope-encoding DNA was added to the 3' end of the rat GnT III cDNA (Nishikawa *et al.*, 1992, *J. Biol. Chem.* 267:18199-18204) by PCR amplification. Nilsson *et al*, 1993, *J. Cell Biol.* 120:5-13. The product was sequenced and subcloned into *pUHD10-3*, a vector for tetracycline-regulated expression (Gossen and Bujard, *supra)* to generate the vector *pUHD10-3-GnT IIIm*. The human GnT V cDNA (Saito *et al.*, 1995, *Eur. J. Biochem.* 233:18-26), was directly subcloned into *pUHD10-3* to generate plasmid vector *pUHD10-3-GnT V*. CHO-tTA cells were co-transfected using a calcium phosphate transfection method (Jordan and Wurm, 1996, *Nucleic Acids Res.* 24:596-601), with *pPur*, a vector for constitutive expression of puromycin resistance (Clontech, Palo Alto, CA), and either the vector *pUHD10-3-GnT IIIm* or the vector *pUHD10-3-GnT V*. Puromycin resistant clones were selected in the presence of tetracycline, isolated and then analyzed for tetracycline-regulated expression of GnT III or GnT V *via* western blots analysis. *See, infra.*

Western And Lectin Blotting. For Western blot analysis of GnT III or GnT V, cell lysates were separated by SDS-PAGE and electroblotted to PVDF membranes (Millipore, Bedford, MA). GnT III was detected using the anti-c-myc monoclonal antibody 9E10 (Nilsson *et al.*, 1993, *J. Cell Biol.* 120:5-13) and GnT V using with an anti-GnT V rabbit polyclonal antibody (Chen *et al.*, 1995, *Glycoconjugate J.* 12:813-823). Anti-mouse or anti-rabbit IgG-horse radish peroxidase (Amersham, Arlington, IL) was used as secondary antibody. Bound secondary antibody was detected using an enhanced chemiluminescence kit (ECL kit, Amersham, Arlington, IL)

For lectin blot analysis of glycoproteins modified either by GnT III- or GnT V-catalyzed reactions, biotinylated E-PHA (Oxford Glycosciences, Oxford, United Kingdom) or L-PHA-digoxigenin (Boehringer Mannheim, Mannheim, Germany), respectively, were used. Merkle and Cummings, 1987. *Methods Enzymol.* 138:232-259.

2. Results And Discussion

Establishment Of CHO Cell Lines With Tetracycline-Regulated Overexpression Of Glycosyl Transferases. The strategy used for establishment of glycosyl transferase overexpressing cell lines consisted of first generating an intermediate CHO cell line constitutively expressing the tetracycline-controlled transactivator (tTA) at an adequate level for the system to work. Yin *et al.*, 1996. *Anal. Biochem.* 235:195-201. This level had to be high enough to activate high levels of transcription, in the absence of tetracycline, from the minimal promoter upstream of the glycosyl transferase genes. CHO cells were co-transfected with a vector for constitutive expression for tTA, driven by the human cytomegalovirus (hCMV) promoter/enhancer, and a vector for expression of a neomycin-resistance (Neo^R) gene. An excess of the tTA-expression vector was used and neomycin-resistant clones were isolated.

In mammalian cells, co-transfected DNA integrates adjacently at random locations within the chromosomes, and expression depends to a large extent on the site of integration and also on the number of copies of intact expression cassettes. A mixed population of clones with different expression levels of the transfected genes is generated. Yin *et al.*, 1996, *supra*. Selection for neomycin resistance merely selects for integration of an intact Neo^R expression cassette, while the use of an excess of the tTA-expression vector increases the probability of finding clones with good expression of tTA. The mixed population of clones has to be screened using a functional assay for tTA expression. Gossen and Bujard, 1992, *supra*; Yin *et al.*, 1996, *supra*. This was done by transfection of each clone with a second vector harboring a reporter gene, *lacZ*, under the control of the tet-promoter and screening for tetracycline-regulated (tet-regulated), transient expression (*i.e.*, one to three days after transfection) of ß-galactosidase activity. CHOt17, which showed the highest level of tet-regulated ß-galactosidase activity among twenty screened clones, was selected for further work.

CHOt17 cells were tested for tet-regulated expression of GnT III by transfecting the cells with vector pUHD10-3-GnT IIIm and comparing the relative levels of GnT III after incubation of the cells in the presence and absence of tetracycline for 36 h. GnT III levels were compared by western blot analysis, using a monoclonal antibody (9E10) which recognizes the c-myc peptide epitope tag at the carboxy-

terminus of GnT III. The tag had been introduced through a modification of the glycosyl transferase gene using PCR amplification. Various reports have demonstrated addition of peptide epitope tags to the carboxy-termini of glycosyl transferases, a group of enzymes sharing the same topology, without disruption of localization or activity. Nilsson *et al.*, 1993, *supra*; Rabouille *et al.*, 1995, *J. Cell Science* 108:1617-1627. FIGURE 2 shows that in clone CHOt17 GnT III accumulation is significantly higher in the absence than in the presence of tetracycline. An additional clone, CHOt2, which gave weaker activation of transcription in the b-galactosidase activity assay, was tested in parallel (FIGURE 2). GnT III and β-galactosidase expression levels follow the same pattern of tetracycline-regulation for both of these clones. The range of tetracycline concentrations where GnT III expression can be quantitatively controlled was found to be from 0 to 100 ng/ml (FIGURE 3). This result agrees with previous research using different cell lines and genes (Yin *et al.*, 1996, *supra*).

To generate a stable cell line with tet-regulated expression of GnT III, CHOtl7 cells were co-transfected with vector pUHD10-3-GnT IIIm and vector, *pPUR*, for expression of a puromycin resistance gene. In parallel, CHOtl7 cells were co-transfected with pUHD10-3-GnT V and *pPUR* vectors to generate an analogous cell line for this other glycosyl transferase. A highly efficient calcium phosphate transfection method was used and the DNA was linearized at unique restriction sites outside the eucaryotic expression cassettes, to decrease the probability of disrupting these upon integration. By using a host in which the levels of tTA expressed had first been proven to be adequate, the probability of finding clones with high expression of the glycosyl transferases in the absence of tetracycline is increased.

Stable integrants were selected by puromycin resistance, keeping tetracycline in the medium throughout clone selection to maintain glycosyl transferase expression at basal levels. For each glycosyl transferase, sixteen puromycin resistant clones were grown in the presence and absence of tetracycline, and eight of each were analysed by western blot analysis (FIGURE 4). The majority of the clones showed good regulation of glycosyl transferase expression. One of the GnT III-expressing clones showed a relatively high basal level in the presence of tetracycline (FIGURE 4B, clone 3), which suggests integration of the expression cassete close to an endogenous CHO-cell enhancer; while two puromycin-resistant clones showed no expression of GnT III in the absence of tetracycline (FIGURE 4B, clones 6 and 8). Among the clones

showing good regulation of expression. different maximal levels of glycosyl transferase were observed. This may be due to variations in the site of integration or number of copies integrated. Activity of the glycosyl transferases was verified by E-PHA and L-PHA lectin binding to endogenous cellular glycoproteins derived from various clones grown in the presence and absence of tetracycline (FIGURE 5). Lectins are proteins which bind to specific oligosaccharide structures. E-PHA lectin binds to bisected oligosaccharides, the products of GnT III-catalyzed reactions, and L-PHA binds to tri- and tetra-antennary oligosaccharides produced by GnT V-catalyzed reactions (Merkle and Cummings, 1987, *Methods Enzymol.* 138:232-259). For each glycosyl transferase, a clone with high expression in the absence, but with undetectable expression in the presence. of tetracycline (clone 6, FIGURE 4A, CHO-tet-GnT V, and clone 4, FIGURE 4B, CHO-tet-GnT IIIm) was selected for further work.

B. Example 2: Inhibition Of Cell Growth Effected By Glycosyl Transferase Overexpresseion

During screening of GnT III- and GnT V-expressing clones in the absence of tetracycline, *see*, Example 1, *supra*, approximately half of each set of clones showed a strong inhibition of growth. The extent of growth-inhibition varied among clones. and comparison with expression levels estimated from western blot analysis (FIGURE 4) suggested a correlation between the degree of growth-inhibition and glycosyl transferase overexpression. This correlation was firmly established by growing the final clones, CHO-tet-GnT IIIm and CHO-tet-GnT V, in different concentrations of tetracycline. A strong inhibition of growth was evident after two days of culture at low levels of tetracycline (FIGURE 6). Growth-inhibited cells displayed a small, rounded morphology instead of the typical extended shape of adherent CHO cells. After a few days, significant cell death was apparent from the morphology of the growth-inhibited cells.

Growth-inhibition due to glycosyl transferase overexpression has not hitherto been reported in the literature, probably due to the widespread use of constitutive promoters. Those clones giving constitutive expression of a glycosyl transferase at growth-inhibiting levels, would be lost during the selection procedure. This was avoided here by keeping tetracycline in the medium, *i.e.*, basal expression levels. throughout selection. Prior to selection, the frequency of clones capable of

expressing glycosyl transferases to growth-inhibiting levels using traditional mammalian vectors based on the constitutive hCMV promoter/enhancer would be expected to be lower. This is due to the fact that, for any given gene, the pUHD10-3 vector in CHO cell lines selected for high constitutive levels of tTA, gives significantly higher expression levels than constitutive hCMV promoter/enhancer-based vectors, as observed by others. Yin *et al.*, 1996, *supra*.

Inhibition of cell growth could be due to a direct effect of overexpression of membrane-anchored, Golgi-resident glycosyl transferases independent of their *in vivo* catalytic activity, *e.g.*, *via* misfolding in the endoplasmic reticulum (ER) causing saturation of elements which assist protein folding in the ER. This could possibly affect the folding and secretion of other essential cellular proteins. Alternatively, inhibition of growth could be related to increased *in vivo* activity of the glycosyl transferase leading to a change of the glycosylation pattern, in a function-disrupting fashion, of a set of endogenous glycoproteins necessary for growth under standard *in vitro* culture conditions.

Independent of the underlying mechanism, the growth-inhibition effect has two consequences for engineering the glycosylation of animal cells. First, it implies that cotransfection of constitutive glycosyl transferase expression vectors together with vectors for the target glycoprotein product is a poor strategy. Other ways of linking expression of these two classes of proteins, *e.g.*, through the use of multiple constitutive promoters of similar strength or use of multicistronic, constitutive expression vectors, should also be avoided. In these cases, clones with very high, constitutive expression of the target glycoprotein, a pre-requisite for an economical bioprocess, would also have high expression of the glycosyl transferase and would be eliminated during the selection process. Linked, inducible expression could also be problematic for industrial bioprocesses, since the viability of the growth-arrested cells would be compromised by the overexpression of the glycosyl transferase.

The second consequence is that it imposes an upper limit on glycosyl transferase overexpression for glycosylation engineering approaches. Clearly, the conversions of many glycosyl transferase-catalyzed reactions in the cell, at the endogenous levels of glycosyl transferases, are very high for several glycosylation sites. However, glycosylation sites where the oligosaccharides are somewhat inaccesible or are stabilized in unfavorable conformations for specific glycosyl tranferases also exist.

For example, it has been observed that addition of bisecting GlcNAc is more restricted to the oligosaccharides attached to the Fc region than to those located on the variable regions of human IgG antibodies. Savvidou *et al.*, 1984, *Biochemistry* 23:3736-3740. Glycosylation engineering of these restricted sites could be affected by such a limit on glycosyl transferase expression. Although this would imply aiming for an "unnatural" distribution of glycoforms, these could be of benefit for special therapeutic applications of glycoproteins.

C. Example 3: Engineering The Glycosylation Of An Anti-Human Neuroblastoma Antibody In Chinese Hamster Ovary Cells

In order to validate the concept of engineering a therapeutic antibody by modifying its glycosylation pattern, a chimeric anti-human neuroblastoma IgG1 (chCE7) was chosen which has insignificant ADCC activity when produced by SP2/0 recombinant mouse myeloma cells. ChCE7 recognizes a tumor-associated 190-kDa membrane glycoprotein and reacts strongly with all neuroblastoma tumors tested to date. It has a high affinity for its antigen ($K_d$of $10^{10}M^{-1}$) and, because of its high tumor-specificity, it is routinely used as a diagnostic tool in clinical pathology. Amstutz *et al.*. 1993. *Int. J. Cancer* 53:147-152. In recent studies, radiolabelled chCE7 has shown good tumor localization in human patients. Dürr, 1993, *Eur. J. Nucl. Med.* 20:858. The glycosylation pattern of chCE7, an anti-neuroblastoma therapeutic monoclonal antibody (mAb) was engineered in CHO cells with tetracycline-regulated expression of GnT III. A set of mAb samples differing in their glycoform distribution was produced by controlling GnT III expression in a range between basal and toxic levels, and their glycosylation profiles were analyzed by MALDI/TOF-MS of neutral oligosaccharides. Measurement of the ADCC activity of these samples showed an optimal range of GnT III expression for maximal chCE7 *in vitro* biological activity, and this activity correlated with the level of Fc-associated bisected, complex oligosaccharides.

1. Materials And Methods

Construction Of chCE7 Expression Vectors. Plasmid vectors 10CE7VH and 98CE7VL, for expression of heavy (IgG1) and light (kappa) chains. respectively, of anti-human neuroblastoma chimeric antibody chCE7, which contain chimeric genomic DNA including the mouse immunoglobulin

promoter/enhancer, mouse antibody variable regions, and human antibody constant regions (Amstutz *et al.*, 1993, *Int. J. Cancer* 53:147-152) were used as starting materials for the construction of the final expression vectors, pchCE7H and pchCE7L. Chimeric heavy and light chain chCE7 genes were reassambled and subcloned into the pcDNA3.1(+) vector. During reassembly, all introns were removed, the leader sequences were replaced with synthetic ones, Reff *et al.*, 1994, *Blood* 83:435-445, and unique restriction sites joining the variable and constant region sequences were introduced. Introns from the heavy constant region were removed by splicing with overlap-extension-PCR. Clackson *et al.*, 1991, General Applications of PCR to Gene Cloning and Manipulation, p. 187-214, *in*: McPherson *et al.* (ed.), PCR a Practical Approach, Oxford University Press, Oxford.

Production Of chCE7 In CHO Cells Expressing Different Levels Of GnT III. CHO-tet-GnT IIIm (*see, supra*) cells were co-transfected with vectors pchCE7H, pchCE7L, and pZeoSV2 (for Zeocin resistance, Invitrogen, Groningen, The Netherlands) using a calcium phosphate transfection method. Zeocin resistant clones were transferred to a 96-well cell culture plate and assayed for chimeric antibody expression using an ELISA assay specific for human IgG constant region. Lifely *et al*, 1995, *supra*. Four chCE7 antibody samples were derived from parallel cultures of a selected clone (CHO-tet-GnT IIIm-chCE7), grown in FMX-8 cell culture medium supplemented with 10% FCS; each culture containing a different level of tetracycline and therefore expressing GnT III at different levels. CHO-tet-GnT IIIm-chCE7 cells were expanded and preadapted to a different concentration of tetracycline during 7 days. The levels of tetracycline were 2000, 60, 30, and 15 ng/ml.

Purification Of chCE7 Antibody Samples. Antibody was purified from culture medium by Protein A affinity chromatography on a 1 ml HiTrap Protein A column (Pharmacia Biotech, Uppsala, Sweden), using linear pH gradient elution from 20 mM sodium phosphate, 20 mM sodium citrate, 500 mM sodium chloride, 0.01% Tween 20, 1M urea, pH 7.5 (buffer A) to buffer B (buffer A without sodium phosphate, pH 2.5). Affinity purified chCE7 samples were buffer exchanged to PBS on a 1 ml ResourceS cation exchange column (Pharmacia Biotech, Uppsala, Sweden). Final purity was judged to be higher than 95% from SDS-PAGE and Coomasie-Blue staining. The concentration of each sample was estimated from the absorbance at 280 nm.

Binding Of Antibodies To Neuroblastoma Cells. Binding affinity to human

neuroblastoma cells was estimated from displacement of ^{125}I-labeled chCE7 by the CHO-produced samples. Amstutz *et al*, 1993, *supra*.

Oligosaccharide Analysis By MALDI/TOF-MS. CE7-2000t, -60t. -30t. and -15t samples were treated with *A. urefaciens* sialidase (Oxford Glycosciences. Oxford, United Kingdom), following the manufacturer's instructions, to remove any sialic acid monosaccharide residues. The sialidase digests were then treated with peptide N-glycosidase F (PNGaseF, Oxford Glycosciences, Oxford, United Kingdom), following the manufacturer's instructions, to release the N-linked oligosaccharides. Protein, detergents, and salts were removed by passing the digests through microcolumns containing, from top to bottom, 20 ml of SepPak C18 reverse phase matrix (Waters, Milford, MA), 20 ml of Dowex AG 50W X8 cation exchange matrix (BioRad, Hercules, CA), and 20 ml of AG 4X4 anion exchange matrix (BioRad, Hercules, CA). The microcolumns were made by packing the matrices in a Gel Loader tip (Eppendorf, Basel, Switzerland) filled with ethanol, followed by an equilibration with water. Küster *et al.*, 1997, *Anal. Biochem.* 250:82-101. Flow through liquid and a 300 ml-water wash were pooled, filtered, evaporated to dryness at room temperature, and resuspended in 2 ml of deionized water. One microliter was applied to a MALDI-MS sample plate (Perseptive Biosystems, Farmingham, MA) and mixed with 1 ml of a 10 mg/ml dehydrobenzoic acid (DHB, Aldrich, Milwakee, Wisconsin) solution in acetonitrile. The samples were air dried and the resulting crystals were dissolved in 0.2 ml of ethanol and allowed to recrystallize by air drying. Harvey, 1993, *Rapid Mass. Spectrom.* 7:614-619. The oligosaccharide samples were then analyzed by matrix-assisted laser desorption ionization/time-of-flight-mass spectrometry (MALDI/TOF-MS) using an Elite Voyager 400 spectrometer (Perseptive Biosystems, Farmingham, MA), equipped with a delayed ion extraction MALDI-ion source, in positive ion and reflector modes, with an accelaration voltage of 20 kV. One hundred and twenty eight scans were averaged. Bisected biantennary complex oligosaccharide structures were assigned to five-HexNAc-associated peaks. Non-bisected tri-antennary N-linked oligosaccharides, the alternative five HexNAc-containing isomers, have never been found in the Fc region of IgGs and their syntheses are catalyzed by glycosyltransferases discrete from GnT III.

ADCC Activity Assay. Lysis of IMR-32 human neuroblastoma cells (target) by human lymphocytes (effector), at a target:effector ratio of 1:19, during a 16 h incubation at 37 °C in the presence of different concentrations of chCE7 samples. was

measured *via* retention of a fluorescent dye. Kolber *et al*, 1988, *J. Immunol. Methods* 108: 255-264. IMR-32 cells were labeled with the fluorescent dye Calcein AM for 20 min (final concentration 3.3 μM). The labeled cells (80'000 cells/well) were incubated for 1h with different concentrations of CE7 antibody. Then, monocyte depleted mononuclear cells were added (1'500'000 cells/well) and the cell mixture was incubated for 16 h at 37°C in a 5% $C0_2$ atmosphere. The supernatant was discarded and the cells were washed once with HBSS and lysed in Triton X-100 (0.1%). Retention of the fluorescent dye in IMR-32 cells was measured with a fluorometer (Perkin Elmer, Luminscence Spectrometer LS 50B, (Foster City, CA) and specific lysis was calculated relative to a total lysis control, resulting from exposure of the target to a detergent instead of exposure to antibody. The signal in the absence of antibody was set to 0% cytotoxicity. Each antibody concentration was analyzed by triplicate, and the assay was repeated three separate times.

2. Results And Discussion

Production Of chCE7 In CHO Cells Expressing Different Levels Of GnT III. ChCE7 heavy and light chain expression vectors were constructed incorporating the human cytomegalovirus (hCMV) promoter, the bovine growth hormone termination and polyadenylation sequences, and eliminating all heavy and light chain introns. This vector design was based on reports of reproducible high-level expression of recombinant IgG genes in CHO cells. Reff *et al.*, 1994, *supra*; Trill *et al.*, 1995, *Current Opinion Biotechnol.* 6:553-560. In addition, a unique restriction sites was introduced in each chain, at the junction between the variable and constant regions. These sites conserve the reading frame and do not change the amino acid sequence. They should enable simple exchange of the mouse variable regions, for the production of other mouse-human chimeric antibodies. Reff *et al.*, 1994, *supra*. DNA sequencing confirmed that the desired genes were appropriately assembled, and production of the chimeric antibody in transfected CHO cells was verified with a human Fc-ELISA assay.

CHO-tet-GnT IIIm-chCE7 cells, with stable, tetracycline-regulated expression of GnT III and stable, constitutive expression of chCE7, were established and scaled-up for production of a set of chCE7 samples. During scale-up, four parallel cultures derived from the same CHO clone were grown, each at a different level of tetracycline and therefore only differing in the level of expression of the GnT III gene.

This procedure eliminates any clonal effects from other variables affecting N-linked glycoform biosynthesis, permitting a rigorous correlation to be established between GnT III gene expression and biological activity of the glycosylated antibody. The tetracycline concentration ranged from 2000 ng/ml, *i.e.*, the basal level of GnT III expression, to 15 ng/ml, at which significant growth inhibition and toxicity due to glycosyl transferase overexpression was observed (*see*, *supra*). Indeed, only a small amount of antibody could be recovered from the latter culture. The second highest level of GnT III expression, using tetracycline at a concentration of 30 ng/ml, produced only a mild inhibition of growth. The purified antibody yield from this culture was approximately 70% that from the remaining two lower levels of GnT III gene overexpression.

The four antibody samples, CE7-2000t, -60t, -30t, and -15t, numbers denoting the associated concentration of tetracycline, were purified by affinity chromatography on Protein A and buffer exchanged to PBS using a cation exchange column. Purity was higher than 95% as judged from SDS-PAGE with Coomassie Blue staining. Binding assays to human neuroblastoma cells revealed high affinity to the cells and no significant differences in antigen binding among the different samples (estimated equilibrium dissociation constants varied between 2.0 and 2.7 x 10^{-10} M). This was as expected, since there are no potential N-linked glycosylation sites in the CE7 variable regions.

Oligosaccharide Distributions And Levels Of Bisected Complex Oligosaccharides Of Different chCE7 Samples. Oligosaccharide profiles were obtained by matrix-assisted laser desorption/ionization mass spectrometry on a time-of-flight instrument (MALDI/TOF-MS). Mixtures of neutral N-linked oligosaccharides derived from each of the four CHO-produced antibody samples and from a SP2/0 mouse myeloma-derived chCE7 (CE7-SP2/0) sample were analyzed using 2,5-dehydrobenzoic acid (2,5-DHB) as the matrix (FIGURE 9). Under these conditions, neutral oligosaccharides appear essentially as single [M + Na^+] ions, which are sometimes accompanied by smaller [M + K^+] ions, depending on the potassium content of the matrix. Bergweff *et al.*, 1995, *Glycoconjugate J.* 12:318-330.

This type of analysis yields both the relative proportions of neutral oligosaccharides of different mass, reflected by relative peak height, and the isobaric monosaccharide composition of each peak. Küster *et al.*, 1997, *supra*; Naven and

Harvey, 1996, *Rapid Commun. Mass Spectrom.* 10:1361-1366. Tentative structures are assigned to peaks based on the monosaccharide composition, knowledge of the biosynthetic pathway, and on previous structural data for oligosaccharides derived from the same glycoprotein produced by the same host, since the protein backbone and the cell type can have a strong influence on the oligosaccharide distribution. Field *et al.*, 1996, *Anal. Biochem.* 239:92-98. In the case of Fc-associated oligosaccharides, only bi-antennary complex oligosaccharides have been detected in IgGs present in human serum or produced by mammalian cell cultures under normal conditions. Wormald *et al.*, 1997, *Biochemistry* 36:1370-1380; Wright and Morrison, 1997, *Tibtech* 15:26-31. The pathway leading to these compounds is illustrated in FIGURE 10, including the mass of the $[M + Na^+]$ ion corresponding to each oligosaccharide. High mannose oligosaccharides have also been detected on antibodies produced in the stationary and death phases of batch cell cultures. Yu Ip *et al.*, 1994, *Arch. Biochem. Biophys.* 308:387-399.

The two major peaks in the CE7-SP2/0 sample (FIGURE 9A) correspond to masses of fucosylated oligosaccharides with four N-acetylhexosamines (HexNAcs) containing either three (m/z 1486) or four (m/z 1648) hexoses. *See*, FIGURE 10, but note that the summarized notation for oligosaccharides in this figure does not count the two GlcNAcs of the core. This composition is consistent with core fucosylated, bi-antennary complex oligosaccharide structures carrying zero or one galactose residues, respectively, typical of Fc-associated oligosaccharides, and as previously observed in NMR analysis of Fc oligosaccharides derived from a chimeric IgG1 expressed in SP2/0 cells. Bergweff *et al.*, 1995, *supra*.

GnT III-catalyzed transfer of a bisecting GlcNAc to these bi-antennary compounds, which are the preferred GnT III acceptors, would lead to oligosaccharides with five HexNAcs (m/z 1689 and 1851, non- and mono-galactosylated, respectively, FIGURE 10), which are clearly absent in the CE7-SP2/0 sample. The latter peaks appear when chCE7 is expressed in CHO-tet-GnTIIIm cells. In the CHO-expressed antibodies the four HexNAc-containing peaks are also mainly fucosylated, although a small amount of non-fucosylated structures is evident from the peak at m/z 1339 (*see*, FIGURE 10). The level of galactosylation is also not very different between the CHO- and SP2/0-derived material. At the basal level of GnT III expression (CE7-2000t sample, FIGURE 9B), the molecules with five HexNAcs are present in a lower

proportion than those with four HexNAcs. A higher level of GnT III expression (CE7-60t sample, FIGURE 9C) led to a reversal of the proportions in favor of oligosaccharides with five HexNAcs. Based on this trend, bisected, bi-antennary complex oligosaccharide structures can be assigned to compounds with five HexNAcs in these samples. Tri-antennary N-linked oligosaccharides, the alternative five HexNAc-containing isomers, have never been found in the Fc region of IgGs and their syntheses are catalyzed by GlcNAc-transferases discrete from GnT III.

A further increase in GnT III expression (CE7-30t sample, FIGURE 9D) did not lead to any significant change in the levels of bisected complex oligosaccharides. Another peak (m/z 1543) containing five HexNAcs appears at low, but relatively constant levels in the CHO-GnTIII samples and corresponds in mass to a non-fucosylated, bisected-complex oligosaccharide mass (FIGURE 10). The smaller peaks at m/z 1705 and 1867, also correspond to five HexNAc-containing bi-antennary complex oligosaccharides. They can be assigned either to potassium adducts of the peaks at m/z 1689 and 1851 (mass difference of 16 Da with respect to sodium adducts) (Küster *et al.*, 1997, *supra*) or to mono- and bi-galactosylated, bisected complex oligosaccharides without fucose (FIGURE 10). Together, the bisected complex oligosaccharides amount to approximately 25% of the total in sample CE7-2000t and reach approximately 45 to 50% in samples CE7-60t and CE7-30t.

Additional information From The Oligosaccharide Profiles Of chCE7 Samples. Although the levels of bisected complex oligosaccharides were not higher in sample CE730t, increased overexpression of GnT III did continue to reduce, albeit to a small extent, the proportions of substrate bi-antennary complex oligosaccharide substrates. This was accompanied by moderate increases in two different, four HexNAc-containing peaks (m/z 1664 and 1810). The latter two peaks can correspond either to galactosylated bi-antennary complex oligosaccharides or to bisected hybrid compounds (FIGURE 11). A combination of both classes of structures is also possible. The relative increase in these peaks is consistent with the accumulation of bisected hybrid by-products of GnT III overexpression. Indeed, the sample produced at the highest level of GnT III overexpression, CE7-15t, showed a large increase in the peak at m/z 1664, a reduction in the peak at m/z 1810 and a concomitant reduction of complex bisected oligosaccharides to a level of approximately 25%. *See*, peaks with m/z 1689 and 1851 in FIGURE 9E and the corresponding structures in FIGURE 11. Higher

accumulation of non-fucosylated (m/z 1664) bisected hybrid by-products. instead of fucosylated ones (m/z 1810), would agree with the fact that oligosaccharides which are first modified by GnT III can no longer be biosynthetic substrates for core α1,6-fucosyltransferase. Schachter, 1986, *Biochem. Cell Biol.* 64:163-181.

The peak at m/z 1257 is present at a level of 10 -15% of the total in the CHO-derived samples and at a lower level in CE7-SP2/0 (FIGURE 9). It corresponds to five hexoses plus two HexNAcs. The only known N-linked oligosaccharide structure with this composition is a five mannose-containing compound of the high-mannose type. Another high mannose oligosaccharide, a six mannose one (m/z 1420), is also present at much lower levels. As mentioned above, such oligosaccharides have been detected in the Fc of IgGs expressed in the late phase of batch cell cultures. Yu lp *et al.*, 1994, *supra*.

Antibody Dependent Cellular Cytotoxicity Of chCE7 Samples. ChCE7 shows some ADCC activity, measured as *in vitro* lysis of neuroblastoma cells by human lymphocytes, when expressed in CHO-tet-GnTIIIm cells with the minimum level of GnT III overexpression (FIGURE 12, sample CE7-2000t). Raising the level of GnT III produced a large increase in ADCC activity (FIGURE 12, sample CE7-60t). Further overexpression of GnT III was not accompanied by an additional increase in activity (FIGURE 12, sample CE7-30t), and the highest level of expression actually led to reduced ADCC (FIGURE 12, sample CE7-15t). Besides exhibiting the highest ADCC activities, both CE7-60t and CE7-30t samples show significant levels of cytotoxicity at very low antibody concentrations. These results show that there is an optimal range of GnT III overexpression in CHO cells for ADCC activity, and comparison with oligosaccharide profiles shows that activity correlates with the level of Fc-associated, bisected complex oligosaccharides.

Given the importance of bisected complex oligosaccharides for ADCC activity, it would be useful to engineer the pathway to further increase the proportion of these compounds. Overexpression of GnT III to levels approaching that used for sample CE7-30t is within the biotechnologically practical range where no significant toxicity and growth inhibiton are observed. At this level of expression, the non-galactosylated, non-bisected, bi-antennary complex oligosaccharides, *i.e.*, the preferred, potential GnT III substrates, are reduced to less than 10% of the total. *See*, m/z 1486 peak, FIGURE 9D. However, only 50% are converted to the desired bisected

biantennary complex structures. The rest are either diverted to bisected, hybrid oligosaccharide byproducts or consumed by the competing enzyme β1,4-galactosyltransferase, GalT (FIGURE 11).

Resolution of the bisected hybrid and the non-bisected, galactosylated complex oligosaccharide peaks by complementary structural analyses would determine how much each potential, undesired route is consuming. The growth of the m/z 1664 and 1810 peaks at high GnT III overexpression levels suggests that at least a fraction of these peaks corresponds to bisected hybrid oligosaccharides (FIGURE 11). In theory, a flux going to bisected hybrid compounds can be reduced by co-overexpression of enzymes earlier in the pathway such as mannosidase II together with GnT III. On the other hand, competition between GnT III and GalT for bisected complex oligosaccharide substrates could potentially be biased towards GnT III-catalyzed reactions, by increasing the intra-Golgi concentration of UDP-GlcNAc while overexpressing GnT III. GnT III transfers a GlcNAc from the co-substrate UDP-GlcNAc to the different oligosaccharides. Should the intra-Golgi concentration of UDP-GlcNAc co-substrate be sub-saturating for GnT III, then increasing it, either by manipulation of the culture medium composition or by genetic manipulation of sugar-nucleotide transport into the Golgi, could favor GnT III in a competition for oligosaccharides with GalT.

It remains to be determined whether the increase in ADCC activity results from the increase in both the galactosylated and non-galactosylated, bisected complex oligosaccharides, or only from one of these forms. *See*, peaks at m/z 1689 and 1851 in FIGURE 9. If it is found that galactosylated, bisected complex bi-antennary oligosaccharides are the optimal structures for increased ADCC activity, then maximizing the fraction of these compounds on the Fc region would require overexpression of both GnT III and GalT. Given the competitive scenario discussed previously, the expression levels of both genes would have to be carefully regulated. In addition, it would be valuable to try to re-distribute overexpressed GalT as much as possible towards the TGN instead of the trans-Golgi cisterna. The latter strategy may be realized by exchanging the transmembrane region-encoding sequences of GalT with those of α2,6-sialyltransferase (Chege and Pfeffer, 1990, *J. Cell. Biol.* 111:893-899).

D. Example 4: Engineering The Glycosylation Of The Anti-CD20 Monoclonal Antibody C2B8

C2B8 is an anti-human CD20 chimeric antibody, Reff, M.E. *et al*, 1994, *supra*. It recieved FDA approval in 1997 and is currently being used, under the comercial name of RituxanTM, for the treatment of Non-Hodgkin's lymphoma in the United States. It is derived from CHO cell culture and therefore should not carry bisected oligosaccharides. *See, supra*. In order to produce an improved version of this antibody, the method demonstrated previously for the chCE7 anti-neuroblastoma antibody was applied. *See, supra*. C2B8 antibody modified according to the disclosed method had a higher ADCC activity than the standard, unmodified C2B8 antibody produced under identical cell culture and purification conditions.

1. Material And Methods

Synthesis Of The Variable Light And Variable Heavy Chain Regions Of Chimeric Anti-CD20 Monoclonal Antibody (C2B8). The VH and VL genes of the C2B8 antibody were assembled synthetically using a set of overlapping single-stranded oligonucleotides (primers) in a one-step process using PCR, Kobayashi *et al*, 1997, *Biotechniques* 23: 500-503. The sequence data coding for mouse immunoglobulin light and heavy chain variable regions (VL and VH respectively) of the anti-CD20 antibody were obtained from a published international patent application (International Publication Number: WO 94/11026). The assembled DNA fragments were subcloned into pBluescriptIIKS(+) and sequenced by DNA cycle sequencing to verify that no mutations had been introduced.

Contruction Of Vectors For Expression Of Chimeric Anti-CD20 Monoclonal Antibody (C2B8). VH and VL coding regions of the C2B8 monoclonal antibody were subcloned in pchCE7H and pchCE7L respectively. In the subcloning, the sequences coding for the variable heavy and light chains of the anti-neuroblastoma CE7 (*see, supra)* were exchanged with the synthetically assembled variable heavy and variable light chain regions of C2B8.

Generation Of CHO-tet-GnTIIIm Cells Expressing C2B8 Antibody. The method for the generation of a CHO-tet-GntIIIm cell line expressing C2B8 antibody was exactly the same as for CHO-tet-GnTIIIm-CE7. *See, supra*. The clone chosen for further work was named CHO-tet-GnTIIIm-C2B8.

Generation Of CHO-tTA Expressing C2B8 Antibody. CHO-tTA is the parental cell line of CHO-tet-GnTIIIm. *See, supra.* The method for the generation of a CHO-tTA cell line expressing C2B8 antibody without GnT III expression was exactly the same as for CHO-tet-GnTIIIm-C2B8 and CHO-tet-GnTIIIm-chCE7. *See, supra.* The clone chosen for further work was named CHO-tTA-C2B8.

Production Of C2B8 Antibody Samples. Two C2B8 antibody samples were derived from parallel CHO-tet-GnTIIIm-C2B8 cultures; each culture containing different levels of tetracycline and therefore expected to express GnTIII at different levels. The levels of tetracycline were 2000, 50, and 25ng/ml. The C2B8 antibody samples derived from these cultures were designated as C2B8-2000t, C2B8-50t, and C2B8-25t, respectively. In parallel, one antibody sample (C2B8-nt) was made from a CHO-tTA-C2B8 culture, this cell line does not express GnT III. CHO-tTA-C2B8 cells were cultured without tetracycline.

Analysis Of GnT III Expression. For Western blot analysis of GnT III, cell lysates of each of the production cultures were resolved by SDS-PAGE and electroblotted to polyvinylidene difluoride membranes. Anti-c-myc monoclonal antibody 9E10 and anti-mouse IgG-horseradish peroxidase (Amersham, Arlington, IL) were used as primary and secondary antibodies respectively. Bound antibody was detected using an enhanced chemiluminiscence kit (Amersham, Arlington, IL).

Purification Of C2B8 Antibody Samples. Antibody samples were purified using the same procedure as for the chCE7 antibody samples. *See, supra.* The concentration was measured using a fluorescence based kit from Molecular Probes (Leiden, The Netherlands).

Verification Of Specific C2B8 Antigen Binding . The specificity of antigen binding of the C2B8 anti-CD20 monoclonal antibody was verified using an indirect immunofluorescence assay with cells in suspension. For this study, CD20 positive cells (SB cells; ATCC deposit no.ATCC CCL120) and CD20 negative cells (HSB cells; ATCC deposit no. ATCC CCL120.1) were utilized. Cells of each type were incubated with C2B8 antibody produced at 25ng/ml tetracycline, as a primary antibody. Negative controls included HBSSB instead of primary antibody. An anti-human IgG Fc specific, polyclonal, FITC conjugated antibody was used for all samples as a secondary antibody (SIGMA, St. Louis, MO). Cells were examined using a Leica (Bensheim, Germany) fluorescence microscope.

ADCC Activity Assay. Lysis of SB cells (CD20+ target cells; ATCC deposit no. ATCC CCL120) by human monocyte depleted peripheral blood mononuclear cells (effector cells) in the presence of different concentrations of C2B8 samples was performed basically following the same procedure described in Brunner *et al.*, 1968, *Immunology* 14:181-189. The ratio of effector cells to target cells was 100:1.

2. Results And Discussion

GnT III Is Expressed At Different Levels In Different Cell Lines And Cultures. The cells of the parallel CHO-tet-GnTIIIm-C2B8 cultures. each culture containing different levels of tetracycline (2000, 50, and 25ng/ml) and therefore expected to express GnTIII at different levels, were lysed and the cell lysates were resolved by SDS-PAGE and detected by Western blotting. The lysates of the culture grown at 25ng/ml tetracycline showed an intense band at the corresponding molecular weight of GnT III whereas cultures grown at 50 and at 2000ng/ml had much less expression of GnT III as shown in FIGURE 13.

Verification Of Specific C2B8 Antigen Binding. C2B8 samples produced from parallel cultures of cells expressing different levels of GnT III were purified from the culture supernatants by affinity chromatography and buffer exchanged to PBS on a cation exchange column. Purity was estimated to be higher than 95% from Coomassie Blue staining of an SDS-PAGE under reducing conditions. These antibody samples were derived from expression of antibody genes whose variable regions were synthesized by a PCR assembly method. Sequencing of the synthetic cDNA fragments revealed no differences to the original C2B8 variable region sequences previously published in an international patent application (International Publication Number WO 94/11026). Specific binding of the samples to human CD20, the target antigen of C2B8, was demonstrated by indirect immunofluorescence using a human lymphoblastoid cell line SB expressing CD20 on its surface and an HSB lymphoblastoid cell line lacking this antigen. Antibody sample C2B8-25t gave positive staining of SB cells (FIGURE 14A), but not of HSB cells under identical experimental conditions (see FIGURE 14B). An additional negative control consisted of SB cells incubated with PBS buffer instead of C2B8-25t antibody. It showed no staining at all.

In Vitro ADCC Activity Of C2B8 Samples. The antibody sample C2B8-nt expressed in CHO-tTA-C2B8 cells that do not have Gnt III expression (*see, supra*)

showed 31% cytotoxic activity (at 1μg/ml antibody concentration), measured as *in vitro* lysis of SB cells (CD20+) by human lymphocytes (FIGURE 15, sample C2B8-nt). C2B8-2000t antibody derived from a CHO-tet-GnTIII culture grown at 2000ng/ml of tetracycline (*i.e.*, at the basal level of cloned GnT III expression) showed at 1μg/ml antibody concentration a 33% increase in ADCC activity with respect to the C2B8-nt sample at the same antibody concentration. Reducing the concentration of tetracycline to 25ng/ml (sample C2B8-25t), which significantly increased GnTIII expression, produced a large increase of almost 80% in the maximal ADCC activity (at 1μg/ml antibody concentration) with respect to the C2B8-nt antibody sample at the same antibody concentration (FIGURE 15, sample C2B8-25t).

Besides exhibiting the highest ADCC activity, C2B8-25t showed significant levels of cytotoxicity at very low antibody concentrations. The C2B8-25t sample at 0.06μg/ml showed an ADCC activity similar to the maximal ADCC activity of C2B8-nt at 1μg/ml. This result showed that sample C2B8-25t, at a 16- fold lower antibody concentration, reached the same ADCC activity as C2B8-nt. This result indicates that the chimeric anti-CD20 antibody C2B8 produced in a cell line actively expressing GnT III was significantly more active than the same antibody produced in a cell line that did not express GnT III.

One advantage of this antibody using the methods of the invention is that (1) lower doses of antibody have to be injected to reach the same therapeutic effect, having a benefical impact in the economics of antibody production, or (2) that using the same dose of antibody a better therapeutic effect is obtained.

E. Example 5: Establishment Of CHO Cell Lines With Constitutive Expression Of Glycosyltransferase Genes At Optimal Levels Leading To Maximal ADCC Activity

In some applications of the method for enhancing the ADCC it may be desirable to use constitutive rather than regulated expression of GnT III on its own or together with other cloned glycosyltransferases and/or glycosidases. However, the inventors have demonstrated that ADCC activity of the modified antibody depends on the expression level of GnT III. *See, supra.* Therefore, it is important to select a clone with constitutive expression of GnT III alone or together with other glycosyltransferase and/or glycosidase genes at optimal or near optimal levels. The optimal levels of

expression of GnT III, either alone or together with other glycosyl transferases such as β(1,4)-galactosyl transferase (GalT), are first determined using cell lines with regulated expression of the glycosyl transferases. Stable clones with constitutive expression of GnT III and any other cloned glycosyltransferase are then screened for expression levels near the optimum.

1. **Determination Of Near-optimal Expression Levels**

Construction Of A Vector For Regulated GnT III Expression linked To GFP Expression. Each glycosyl transferase gene is linked, *via* an IRES sequence, to a reporter gene encoding a protein retained in the cell, *e.g.*, green fluorescent protein (GFP) or a plasma membrane protein tagged with a peptide that can be recognized by available antibodies. If more than one glycosyl transferase is being tested, a different marker is associated with each glycosyl transferase, *e.g.*, GnT III may be associated to GFP and GalT may be associated to blue fluorescent protein (BFP). An eucaryotic expression cassette consisting of the GnT III cDNA upstream of an IRES element upstream of the GFP cDNA is first assembled by standard subcloning and/or PCR steps. This cassette is then subcloned in the tetracycline regulated expression vector pUHD10-3 (*see, supra*), downstream of the tet-promoter and upstream of the termination and polyadenylation sequences resulting in vector pUHD10-3-GnTIII-GFP.

Establishment Of CHO Cells With Regulated GnTIII Expression Linked To GFP Expression And Constitutive chCE7 Antibody Expression. CHO-tTA cells (*see, supra*) expressing the tetracycline-responsive transactivator, are co-transfected with vector pUHD10-3-GnTIII-GFP and vector pPur for expression of a puromycin-resistance gene. *See, supra.* Puromycin resistant clones are selected in the presence of tetracycline. Individual clones are cultured by duplicate in the presence (2μg/ml) or absence of tetracycline. Six clones that show inhibition of growth in the absence of tetracycline, due to glycosyltransferase overexpression (*see, supra*), are selected and analyzed by fluorescence-activated cell sorting (FACS) for detection of the GFP-associated signal. A clone giving the highest induction ratio, defined as the ratio of fluorescence in the absence of tetracycline to fluorescence in the presence of tetracycline is chosen for further work and designated as CHO-tet-GnTIII-GFP. CHO-tet-GnTIII-GFP are transfected with expression vectors for antibody chCE7 and a clone with high constitutive expression of this antibody is selected CHO-tet-GnTIII-GFP-

chCE7. *See, supra.*

Production Of chCE7 Samples, Measurement Of ADCC Activity And Determination Of Optimal GnTIII Expression Levels. Parallel cultures of CHO-tet-GnTIII-GFP-chCE7 are grown at different levels of tetracycline, and therefore expressing GnTIII together with GFP at different levels. chCE7 antibody samples are purified from the culture supernatants by affinity chromatography. In parallel, the cells from each culture are analyzed by FACS to determine the mean level of GFP-associated fluorescence, which is correlated to the expression level of GnT III, of each culture. The *in vitro* ADCC activity of each chCE7 antibody sample is determined (*see. supra*) and the maximal *in vitro* ADCC activity of each sample is plotted against the mean fluorescence of the cells used to produce it.

2. Establishment Of A CHO Cell Line With Constitutive GnTIII expression At Near-optimal Levels

The GnTIII-IRES-GFP cassette (*see, supra*) is subcloned in a constitutive expression vector. CHO cells are stably co-transfected with this vector and a vector for puromycin resistance. Puromycin resistant cells are selected. This population of stably transfected cells is then sorted *via* FACS, and clones are selected which express the levels of reporter GFP gene near the within the range where optimal or near-optimal ADCC activity is achieved. *See, supra*. This final transfection step may be done either on CHO cells already stably expressing a therapeutic antibody or on empty CHO cells, *e.g.*, DUKX or DG44 dhfr- CHO cells. In the latter case, the clones obtained from the procedure described above will be transfected with therapeutic antibody-expression vectors in order to generate the final antibody-producing cell lines.

F. Example 6: Cell Surface Expression Of A Human IgG Fc Chimera With Optimized Glycosylation

Encapsulated cell therapy is currently being tested for a number of diseases. An encapsulated cell implant is designed to be surgically placed into the body to deliver a desired therapeutic substance directly where it is needed. However, if once implanted the encapsulated device has a mechanical failure, cells can escape and become undesirable. One way to destroy escaped, undesirable cells in the body is *via* an Fc-mediated cellular cytoxicity mechanism. For this purpose, the cells to be

encapsulated can be previously engineered to express a plasma membrane-anchored fusion protein made of a type II transmembrane domain that localizes to the plasma membrane fused to the N-terminus of an Fc region. Stabila, P.F., 1998, *supra*. Cells inside the capsule are protected against Fc-mediated cellular cytoxicity by the capsule, while escaped cells are accesible for destruction by lymphocytes which recognize the surface-displayed Fc regions, *i.e.*, *via* an Fc-mediated cellular cytoxicity mechanism. This example illustrates how this Fc-mediated cellular cytoxicity activity is enhanced by glycosylation engineering of the displayed Fc regions.

1. Establishment Of Cells Expressing The Fc Chimera On Their Surface And Expressing GnTIII

Cells to be implanted for a particular therapy, for example baby hamster kidney (BHK) cells, which already produce the surface-displayed Fc chimera and a secreted, therapeutic protein, are first stably transfected with a vector for constitutive expression of GnTIII linked *via* an IRES element to expression of GFP. *See, supra*. Stable transfectants are selected by means of a marker incorporated in the vector, *e.g.*, by means of a drug resistance marker and selected for survival in the presence of the drug.

2. Screening Of Cells Expressing Diffent Levels Of GnTIII And Measurement

Stable transfectants are analyzed by fluorescence-activated cell sorting (FACS) and a series of clones with different mean fluorescence levels are selected for further studies. Each selected clone is grown and reanalyzed by FACS to ensure stability of GFP, and therefore associated GnT III, expression.

3. Verification Of Different Levels Of Bisected Complex Oligosaccharides On The Displayed Fc Regions

Fc regions from three clones with different levels of GFP-associated fluorescence and from the original BHK cells not transfected with the GnTIII-IRES-GFP vector are solubilized from the membrane by means of a detergent and then purified by affinity chromatography. The oligosaccharides are then removed, purified and analyzed by MALDI-TOF/MS. *See, supra*. The resulting MALDI-TOF/MS profiles show that the Fc-regions of the modified, fluorescent clones carry

different proportions of bisected complex oligosaccharides. The MALDI profile from the unmodified cells does not show any peak associated to bisected oligosaccharides. The clone with carrying the highest levels of bisected complex oligosaccharides on the displayed Fc regions is chosen for further work.

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4. *In vitro* Fc-mediated Cellular Cytoxicity Activity Assay

Two Fc-mediated cellular cytoxicity activity assays are then conducted in parallel. In one assay the target cells are derived from the clone selected above. In the parallel assay the target cells are the original cells to be encapsulated and 10 which have not been modified to express GnTIII. The assay is conducted using the procedure described previously (*see, supra*) but in the absence of any additional antibody, since the target cells already display Fc regions. This experiment demonstrates that the Fc-mediated cellular cytoxicity activity against the cells expressing GnT III is higher than that against cells not expressing this 15 glycosyltransferase.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

CLAIMS

What is claimed is:

1. A host cell engineered to express at least one nucleic acid encoding a glycoprotein-modifying glycosyl transferase at a regulated level.

2. The host cell of Claim 1, wherein a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced in said host cell.

3. The host cell of Claim 1, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

4. The host cell of Claim 2 or 3, wherein said host cell is a CHO cell, a BHK cell, a NS0 cell, a SP2/0 cell, or a hybridoma cell.

5. The host cell of Claim 3, wherein said endogenous glycoprotein-modifying glycosyl transferase has been activated by insertion of a regulated promoter element into the host cell chromosome.

6. The host cell of Claim 2 or 3, wherein said glycoprotein-modifying glycosyl transferase is GnT III, GnT V, Man II, or Gal T.

7. The host cell of Claim 2 or 3, wherein said host cell is engineered to express at least two different glycoprotein-modifying glycosyl transferases selected from the group consisting of GnT III, GnT V, Man II, and Gal T.

8. The host cell of Claim 7, wherein at least one gene encoding a glycoprotein-modifying glycosyl transferase is operably linked to a constitutive promoter element.

9. The host cell of Claim 2, wherein at least one gene encoding a

glycoprotein-modifying glycosyl transferase is operably linked to a regulated promoter element.

10. The host cell of Claim 5 or 9, wherein the regulated promoter element is a tetracycline-regulated promoter system, an ecdysone-inducible promoter system, a lac-switch promoter system, a glucocorticoid-inducible promoter system, a temperature-inducible promoter system, or a metallothionein metal-inducible promoter system.

11. A host cell engineered to express at least one nucleic acid molecule encoding a glycoprotein-modifying glycosyl transferase, wherein said host cell is capable of producing a protein having enhanced Fc-mediated cellular cytotoxicity.

12. The host cell of Claim 11, wherein said protein is a whole antibody molecule, an antibody fragment, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin.

13. The host cell of Claim 12, wherein a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced into said host cell chromosome.

14. The host cell of Claim 12, wherein said host cell has been selected to carry a mutation triggering expression of an endogenous glycoprotein-modifying glycosyl transferase.

15. The host cell of Claim 14, wherein said host cell is the mutant lec10.

16. The host cell of Claim 12, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

17. The host cell of Claim 16, wherein said endogenous glycoprotein-modifying glycosyl transferase has been activated by insertion of a regulated promoter element into the host cell chromosome.

18. The host cell of Claim 16, wherein said endogenous glycoprotein-modifying glycosyl transferase has been activated by insertion of a constitutive promoter element, a transposon, or a retroviral element into the host cell chromosome.

19. The host cell of Claim 11 or 13, further comprising at least one transfected nucleic acid encoding an antibody molecule, an antibody fragment, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin.

20. The host cell of Claim 13, wherein at least one gene encoding a glycoprotein-modifying glycosyl transferase is operably linked to a constitutive promoter element.

21. The host cell of Claim 13, wherein at least one gene encoding a glycoprotein-modifying glycosyl transferase is operably linked to a regulated promoter element.

22. The host cell of Claim 21, wherein the regulated promoter element is a tetracycline-regulated promoter system, an ecdysone-inducible promoter system, a lac-switch promoter system, a glucocorticoid-inducible promoter system, a temperature-inducible promoter system, or a metallothionein metal-inducible promoter system.

23. The host cell of Claim 11, wherein said host cell is a hybridoma cell.

24. The host cell of Claim 11, wherein said engineered host cell is an engineered CHO cell, an engineered BHK cell, an engineered NS0 cell, or an engineered SP2/0 cell.

25. The host cell of Claim 11, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-CD20 monoclonal antibody (C2B8).

26. The host cell of Claim 11, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-human neuroblastoma monoclonal

antibody (chCE7).

27. The host cell of Claim 11, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-human renal cell carcinoma monoclonal antibody (ch-G250), a humanized anti-HER2 monoclonal antibody, a chimeric anti-human colon, lung, and breast carcinoma monoclonal antibody (ING-1), a humanized anti-human 17-1A antigen monoclonal antibody (3622W94), a humanized anti-human colorectal tumor antibody (A33), an anti-human melanoma antibody (R24) directed against GD3 ganglioside, or a chimeric anti-human squamous-cell carcinoma monoclonal antibody (SF-25).

28. The host cell of Claim 11, wherein at least one nucleic acid molecule encodes ß(1,4)-N-acetylglucosaminyltransferase III (GnT III).

29. The host cell of Claim 28, further comprising at least one nucleic acid encoding a ß(1,4)-galactosyl transferase (GalT).

30. The host cell of Claim 28, further comprising at least one nucleic acid encoding a mannosidase II (Man II).

31. The host cell of Claim 28, further comprising at least one nucleic acid encoding a β(1,4)-galactosyl transferase (GalT) and at least one nucleic acid encoding a mannosidase II (Man II).

32. A method for producing a protein compound having enhanced Fc-mediated cellular cytotoxicity in a host cell, comprising:

(a) providing a host cell engineered to express a glycoprotein-modifying glycosyl transferase at a regulated level, chosen to improve glycosylation of a protein compound of interest, wherein said host cell expresses at least one nucleic acid encoding an antibody, an antibody fragment, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin;

(b) culturing said host cell under conditions which permit the production of said protein compound having enhanced Fc-mediated dependent cellular

cytotoxicity; and

(c) isolating said protein compound having enhanced Fc-mediated cellular cytotoxicity.

33. The method of Claim 32, wherein in step (a), said host cell comprises at least one nucleic acid encoding a whole antibody.

34. The method of Claim 32, wherein in step (a), said host cell comprises at least one nucleic acid encoding an antibody fragment.

35. The method of Claim 32, wherein in step (a), said host cell comprises at least one nucleic acid encoding a fusion protein comprising a region resembling a glycosylated Fc region of an immunoglobulin.

36. The method of Claim 32, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-CD20 monoclonal antibody (C2B8).

37. The method of Claim 32, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-human neuroblastoma monoclonal antibody (chCE7).

38. The method of Claim 32, wherein said host cell comprises at least one transfected nucleic acid encoding a chimeric anti-human renal cell carcinoma monoclonal antibody (ch-G250), a humanized anti-HER2 monoclonal antibody, a chimeric anti-human colon, lung, and breast carcinoma monoclonal antibody (ING-1), a humanized anti-human 17-1A antigen monoclonal antibody (3622W94), a humanized anti-human colorectal tumor antibody (A33), an anti-human melanoma antibody (R24) directed against GD3 ganglioside, or a chimeric anti-human squamous-cell carcinoma monoclonal antibody (SF-25).

39. The method of Claim 32, wherein with at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced into said host cell.

40. The host cell of Claim 32, wherein said host cell has been selected to carry a mutation triggering expression of an endogenous glycoprotein-modifying glycosyl transferase.

41. The host cell of Claim 40, wherein said host cell is the mutant lec10.

42. The host cell of Claim 32, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

43. The method of Claim 32, wherein said glycosyl transferase is a ß(1,4)-N-acetylglucosaminyltransferase III (GnT III).

44. The method of Claim 43, wherein said GnT III is expressed using a constitutive promoter system.

45. The method of Claim 43, wherein said GnT III is expressed using a regulated promoter system.

46. The method of Claim 45, wherein said regulated promoter system is a tetracycline-regulated promoter system, an ecdysone-inducible promoter system, a lac-switch promoter system, a glucocorticoid-inducible promoter system, a temperature-inducible promoter system, or a metallothionein metal-inducible promoter system.

47 The method of Claim 32, wherein said glycosyl transferase is a β(1,4)-galactosyl transferase (GalT).

48. The method of Claim 47, wherein said GalT is expressed using a constitutive promoter system.

49. The method of Claim 47, wherein said GalT is expressed using a regulated promoter system.

50. The method of Claim 49, wherein said regulated promoter system is

a tetracycline-regulated promoter system, an ecdysone-inducible promoter system, a lac-switch promoter system, a glucocorticoid-inducible promoter system, a temperature-inducible promoter system, or a metallothionein metal-inducible promoter system.

51. The method of Claim 32, wherein said host cell is engineered to express a plurality of nucleic acids encoding a glycosyl transferase at a regulated level, chosen to improve glycosylation of a protein compound of interest, wherein at least one nucleic acid encodes GnT III and at least one nucleic acid encodes a β(1,4)-galactosyl transferase (GalT).

52. The host cell of Claim 51, wherein a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced into said host cell.

53. The host cell of Claim 51, wherein said host cell has been selected to carry a mutation triggering expression of at least one endogenous glycoprotein-modifying glycosyl transferase.

54. The host cell of Claim 51, 52, or 53, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

55. The method of Claim 32, wherein said host cell comprises a plurality of nucleic acids encoding a glycoprotein-modifying glycosyl transferase at a regulated level, chosen to improve glycosylation of a protein compound of interest, wherein at least one nucleic acid encodes GnT III and at least one nucleic acid encodes a mannosidase II (Man II).

56. The host cell of Claim 55, wherein a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced into said host cell.

57. The host cell of Claim 55, wherein said host cell has been selected to

carry a mutation triggering expression of at least one endogenous glycoprotein-modifying glycosyl transferase.

58. The host cell of Claim 55, 56, or 57, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

59. The method of Claim 32, wherein said host cell comprises a plurality of nucleic acids encoding a glycoprotein-modifying glycosyl transferase at a regulated level, chosen to improve glycosylation of a protein of interest, wherein at least one nucleic acid encodes GnT III, at least one nucleic acid encodes β(1,4)-galactosyl transferase (GalT), and at least one nucleic acid encodes mannosidase II (Man II).

60. The host cell of Claim 59, wherein a nucleic acid molecule comprising at least one gene encoding a glycoprotein-modifying glycosyl transferase has been introduced into said host cell.

61. The host cell of Claim 59, wherein said host cell has been selected to carry a mutation triggering expression of at least one endogenous glycoprotein-modifying glycosyl transferase.

62. The host cell of Claim 59, 60, or 61, wherein said host cell has been engineered such that an endogenous glycoprotein-modifying glycosyl transferase is activated.

63. The method of Claim 32, wherein the expression level of at least one glycoprotein-modifying glycosyl transferase has been selected to produce an antibody molecule, an antibody fragment, or a fusion protein that includes a region equivalent to the Fc region of an immunoglobulin having enhanced Fc-mediated cellular cytotoxicity at a higher level than the Fc-mediated cellular cytotoxicity obtained from a different expression level of the same glycosyl transferase gene.

64. The method of Claim 63, wherein said expression levels are

determined by Western blot analysis using a glycosyl transferase-specific antibody.

65. The method of Claim 63, wherein said expression levels are determined by Northern blot analysis using a glycosyl transferase-specific probe.

66. The method of Claim 63, wherein said expression levels are determined by measuring the enzymatic activity of glycosyl transferase.

67. The method of Claim 63, wherein said expression levels are determined using a lectin which binds to biosynthetic products of glycoprotein-modifying glycosyl transferase.

68. The method of Claim 67, wherein the lectin is E_4-PHA lectin.

69. The method of Claim 63, wherein said nucleic acid encoding said glycoprotein-modifying glycosyl transferase is operatively linked to a reporter gene, and wherein said expression levels of said glycosyl transferase are determined by measuring a signal correlated with the expression level of said reporter gene.

70. The method of Claim 69, wherein said reporter gene is transcribed together with at least one nucleic acid encoding said glycoprotein-modifying glycosyl transferase as a single RNA molecule and their respective coding sequences are linked either by an internal ribosome entry site (IRES) or by a cap-independent translation enhancer (CITE).

71. The method of Claim 69, wherein said reporter gene is translated together with at least one nucleic acid encoding said glycoprotein-modifying glycosyl transferase such that a single polypeptide chain is formed.

72. The method of Claim 63, wherein said nucleic acid encoding said glycoprotein-modifying glycosyl transferase is operatively linked to a reporter gene under the control of a single promoter, wherein said nucleic acid encoding said glycoprotein-modifying glycosyl transferase and said reporter gene are transcribed into

an RNA molecule which is alternatively spliced into two separate messenger RNA (mRNA) molecules, wherein one of the resulting mRNAs is translated into said reporter protein, and the other is translated into said glycoprotein-modifying glycosyl transferase.

73. The method of Claim 32, wherein said host cell further comprises a nucleic acid encoding a glycosidase.

74. An antibody having enhanced antibody dependent cellular cytotoxicity (ADCC) produced by the host cells of Claim 11.

75. A chimeric anti-CD20 monoclonal antibody (C2B8) having enhanced antibody dependent cellular cytotoxicity (ADCC) produced by the host cells of Claim 25.

76. A chimeric anti-human neuroblastoma monoclonal antibody (chCE7) having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 26.

77. A chimeric anti-human renal cell carcinoma monoclonal antibody (ch-G250) having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

78. A humanized anti-HER2 monoclonal antibody having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

79. A chimeric anti-human colon, lung, and breast carcinoma monoclonal antibody (ING-1) having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

80. A humanized anti-human 17-1A antigen monoclonal antibody (3622W94) having enhanced antibody dependent cellular cytotoxicity (ADCC)

produced using the host cells of Claim 27.

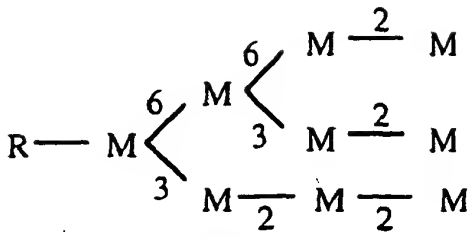
81. A chimeric anti-human squamous-cell carcinoma monoclonal antibody (SF-25) having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

82. A humanized anti-human colorectal tumor antibody (A33), having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

83. An anti-human melanoma antibody (R24) directed against GD3 ganglioside, having enhanced antibody dependent cellular cytotoxicity (ADCC) produced using the host cells of Claim 27.

84. An antibody fragment that includes a region equivalent to the Fc region of an immunoglobulin, having enhanced Fc-mediated cellular cytotoxicity produced using the host cells of Claim 11.

85. A fusion protein that includes a region equivalent to the Fc region of an immunoglobulin, having enhanced Fc-mediated cellular cytotoxicity produced using the host cells of Claim 11.



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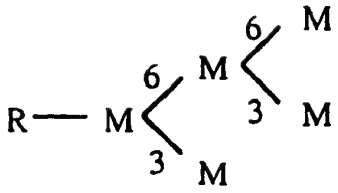
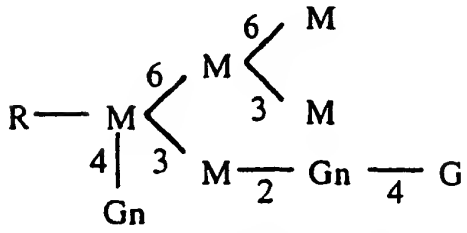
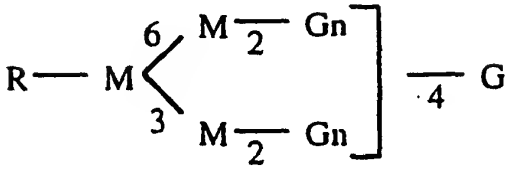


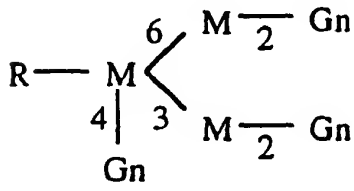
M_5. High-mannose



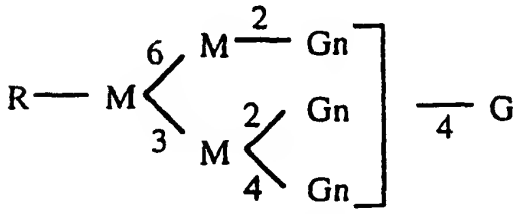
M_5GnGn^bG. Bisected hybrid



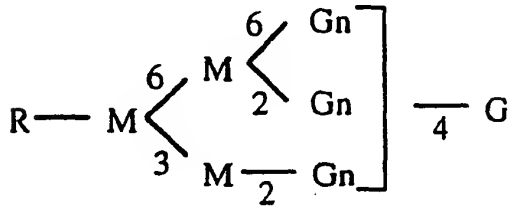
M_3Gn_2G. Bi-antennary complex



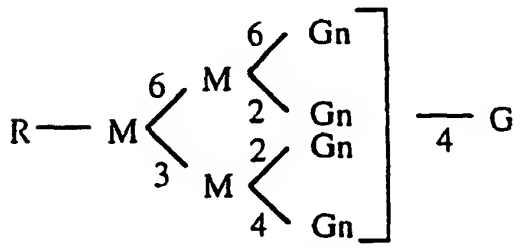
$M_3Gn_2Gn^b$. Bisected bi-antennary complex



M_3Gn_3G. Tri-antennary complex



$M_3Gn_3'G$. Tri'-antennary complex



M_3Gn_4G. Tetra-antennary complex

FIG.1

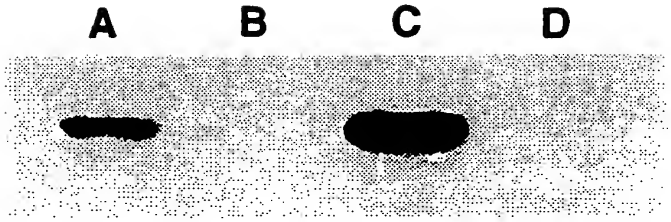


FIG.2

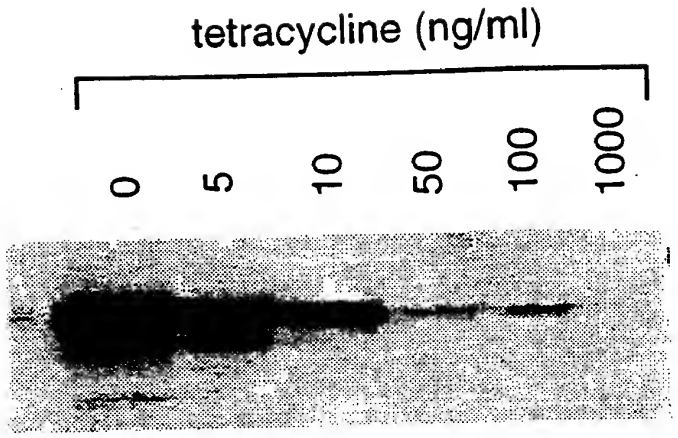


FIG.3

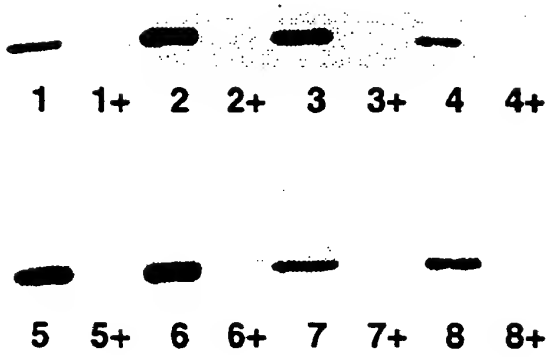


FIG.4A

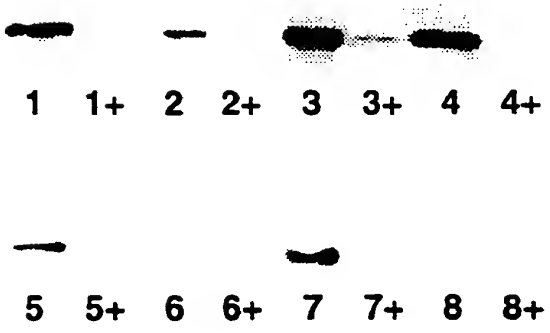


FIG.4B

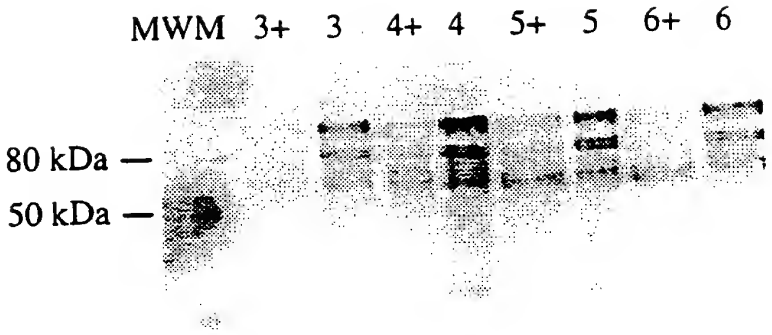


FIG.5A

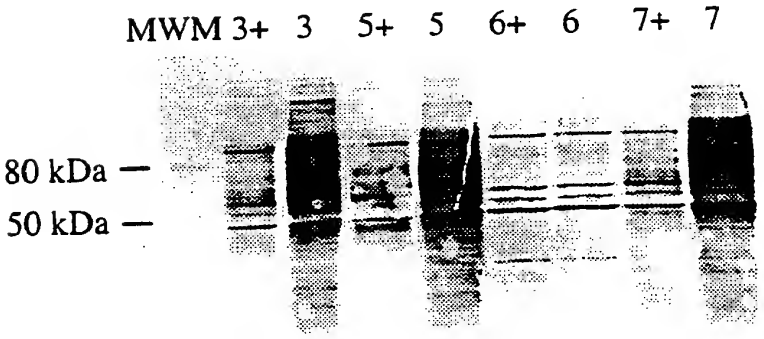


FIG.5B

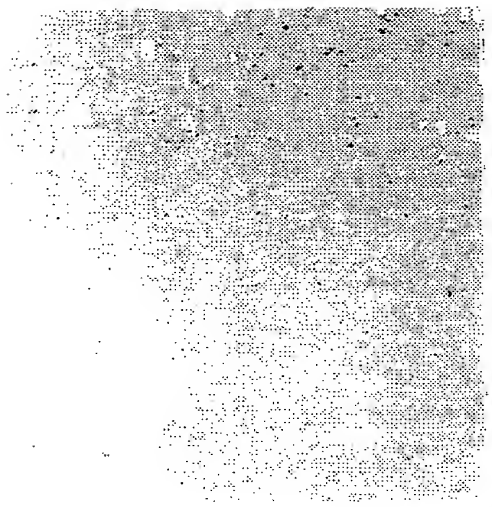


FIG.6A

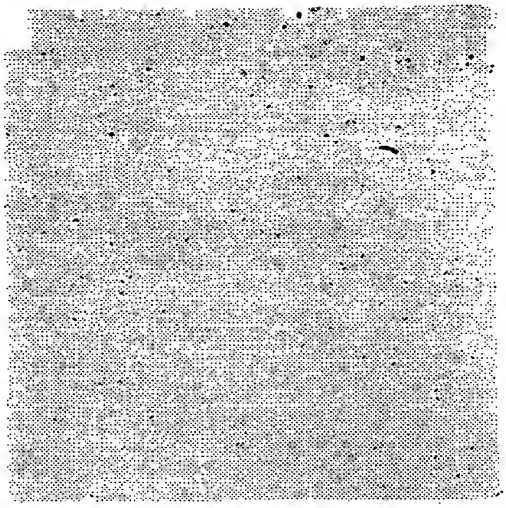


FIG.6B

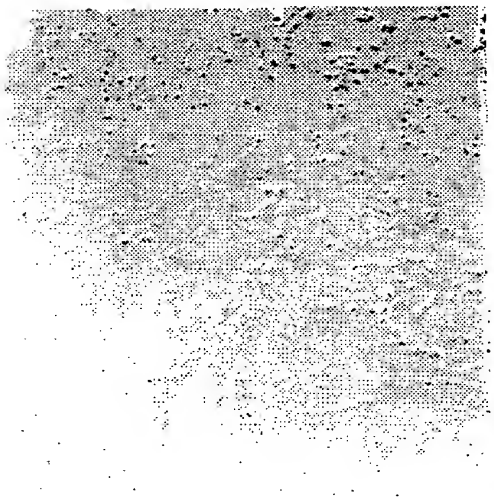


FIG.6C

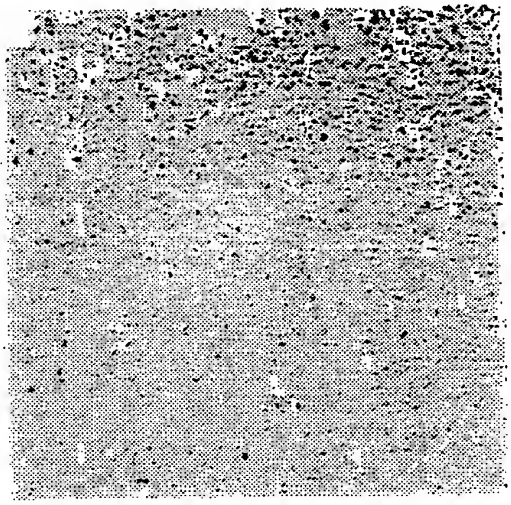


FIG.6D

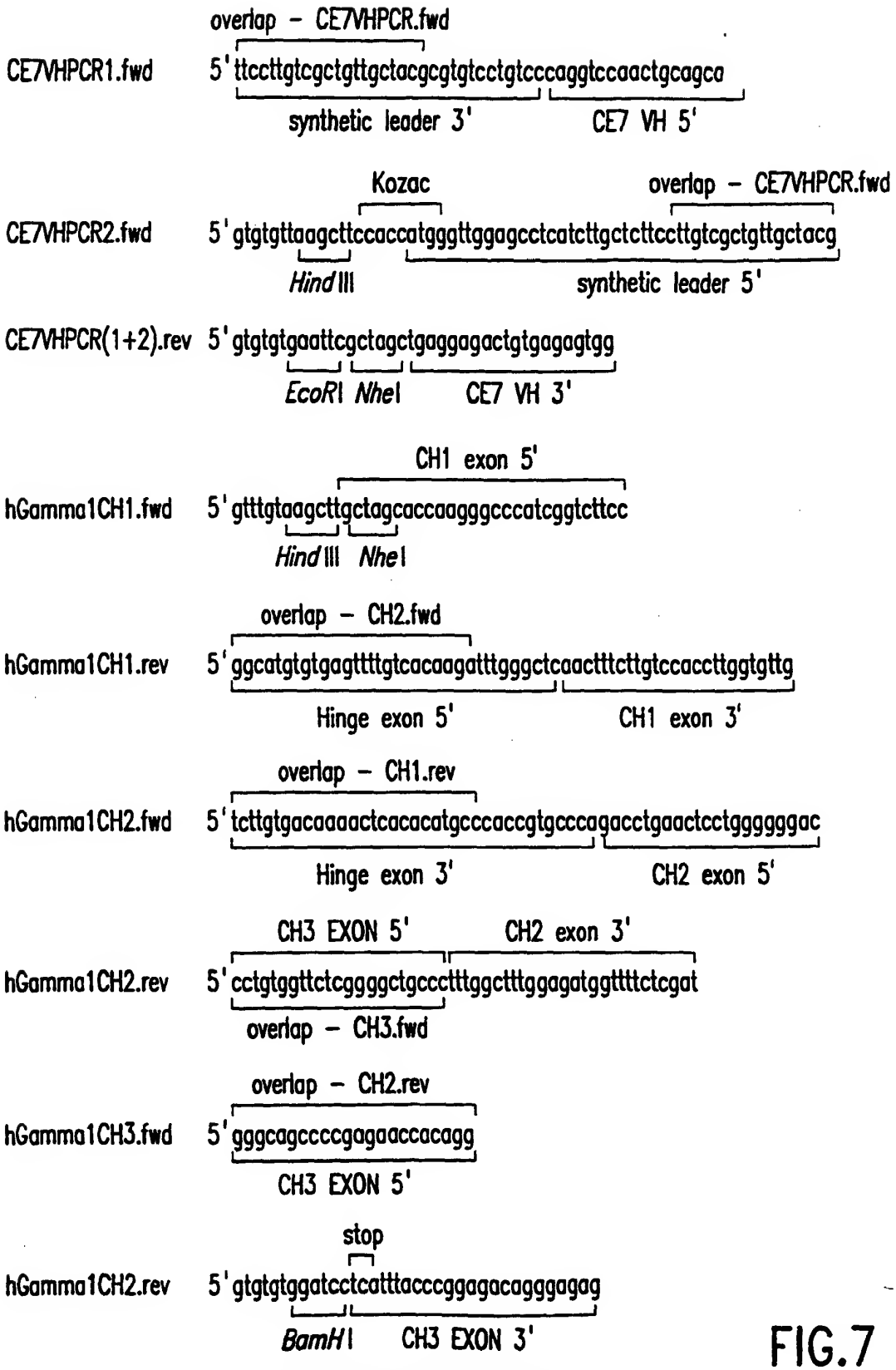
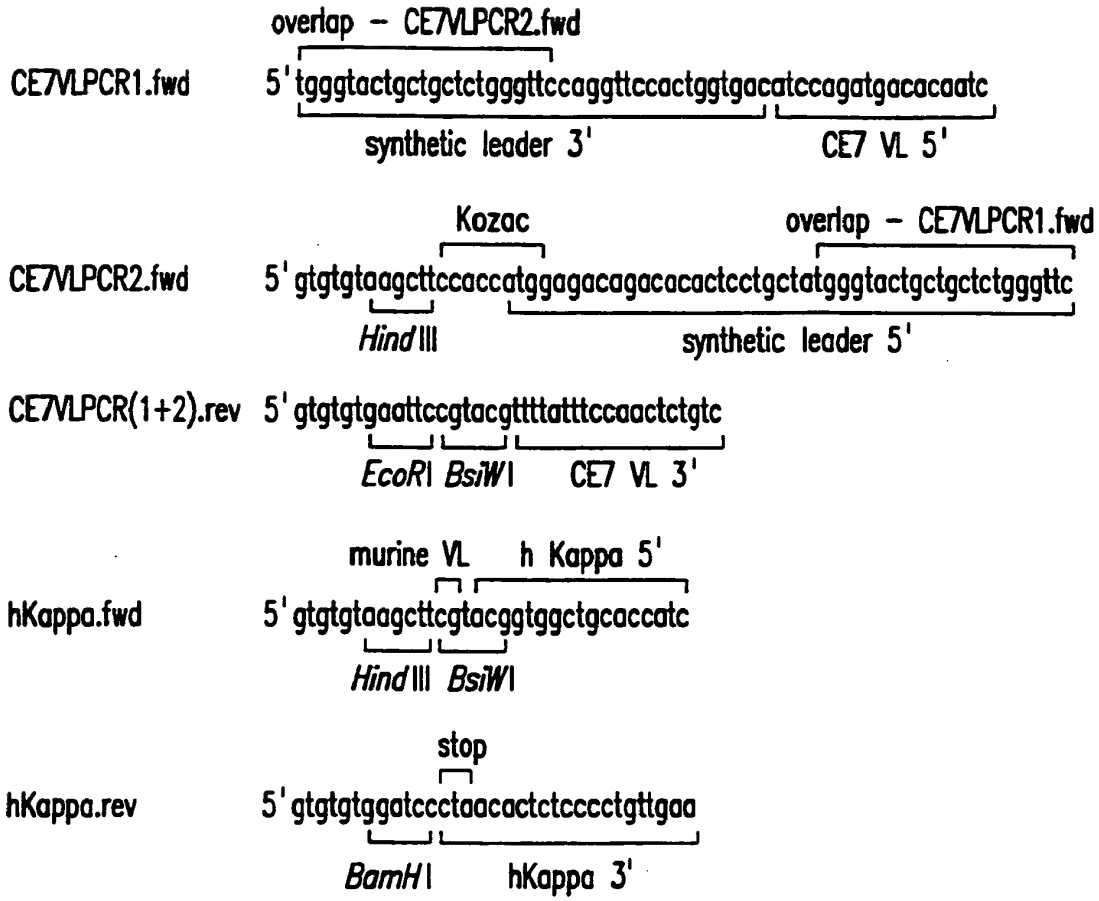


FIG.7


overlap – CE7VLPCR2.fwd
CE7VLPCR1.fwd
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synthetic leader 3'
CE7 VL 5'
Kozac
overlap – CE7VLPCR1.fwd
CE7VLPCR2.fwd
5' gtgtgtaagcttccaccatggagacagacacactcctgctatgggtactgctgctctgggttc
HindIII
synthetic leader 5'
CE7VLPCR(1+2).rev
5' gtgtgtgaattccgtacgttttatttccaactctgtc
EcoRI BsiWI
CE7 VL 3'
murine VL
h Kappa 5'
hKappa.fwd
5' gtgtgtaagcttcgtacggtggctgcaccatc
HindIII BsiWI
stop
hKappa.rev
5' gtgtgtggatccctaacactctcccctgttgaa
BamHI
hKappa 3'

FIG.8

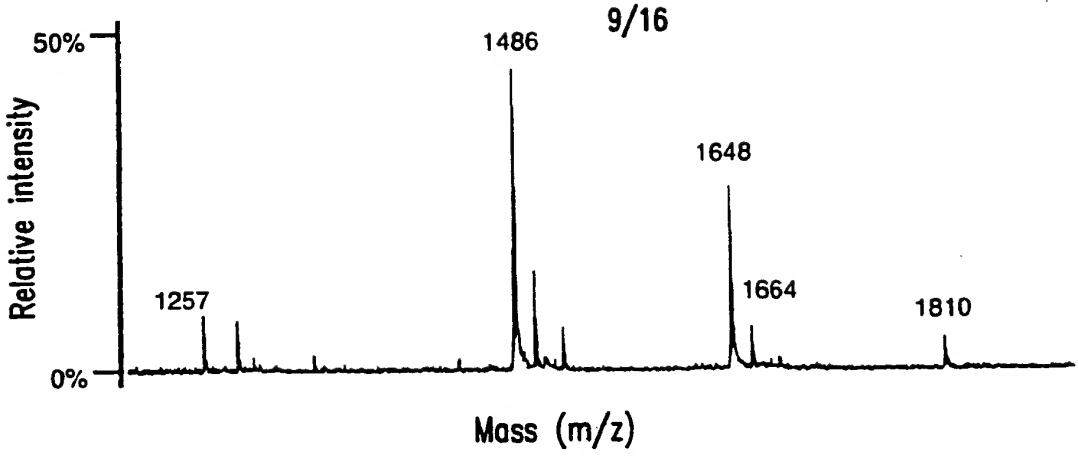

FIG.9A

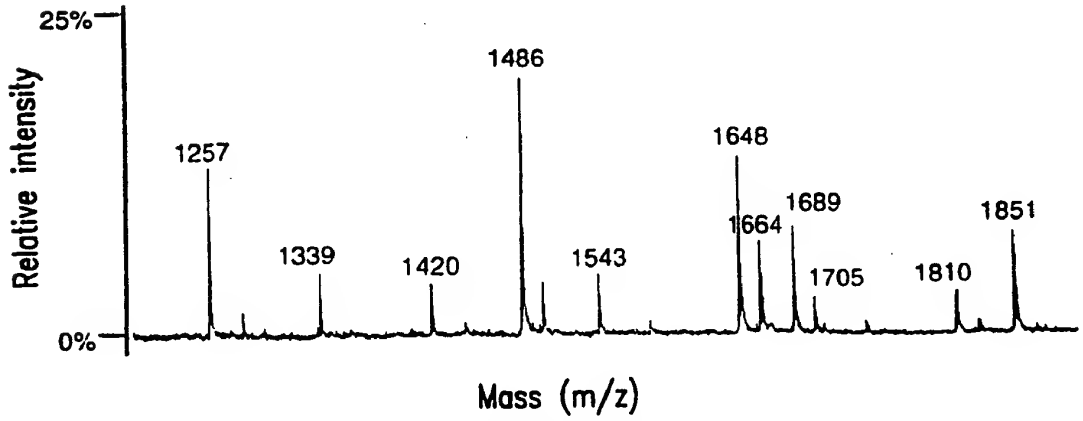

FIG.9B

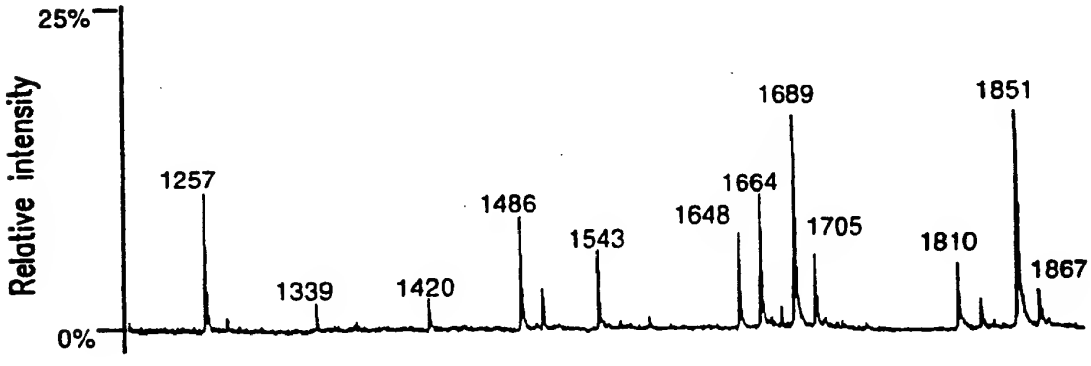

FIG.9C

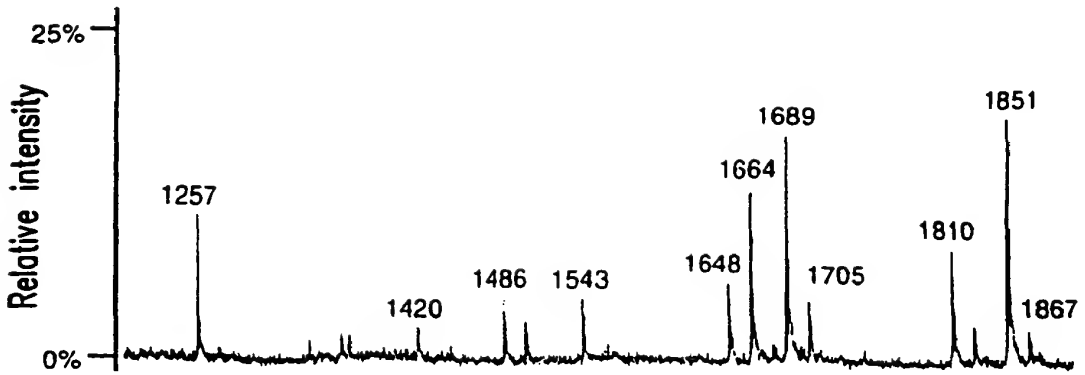

FIG.9D

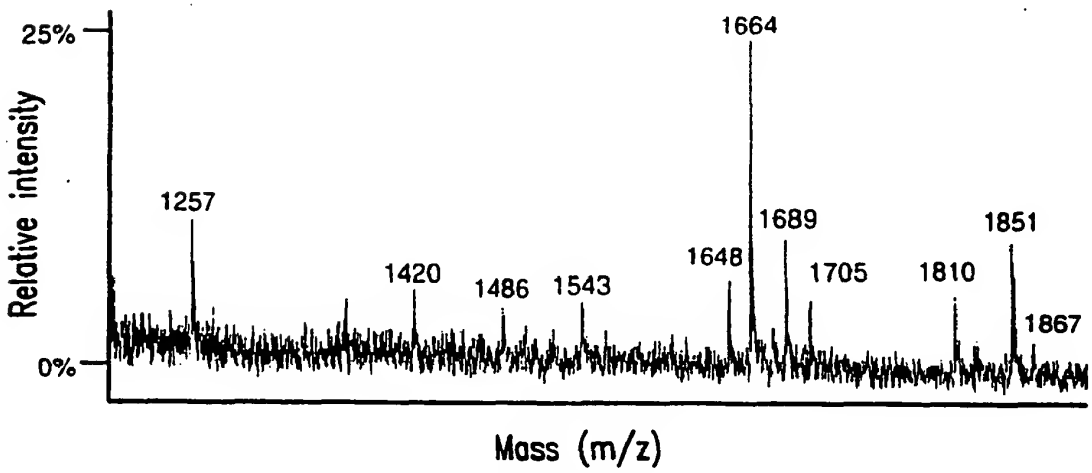

FIG.9E

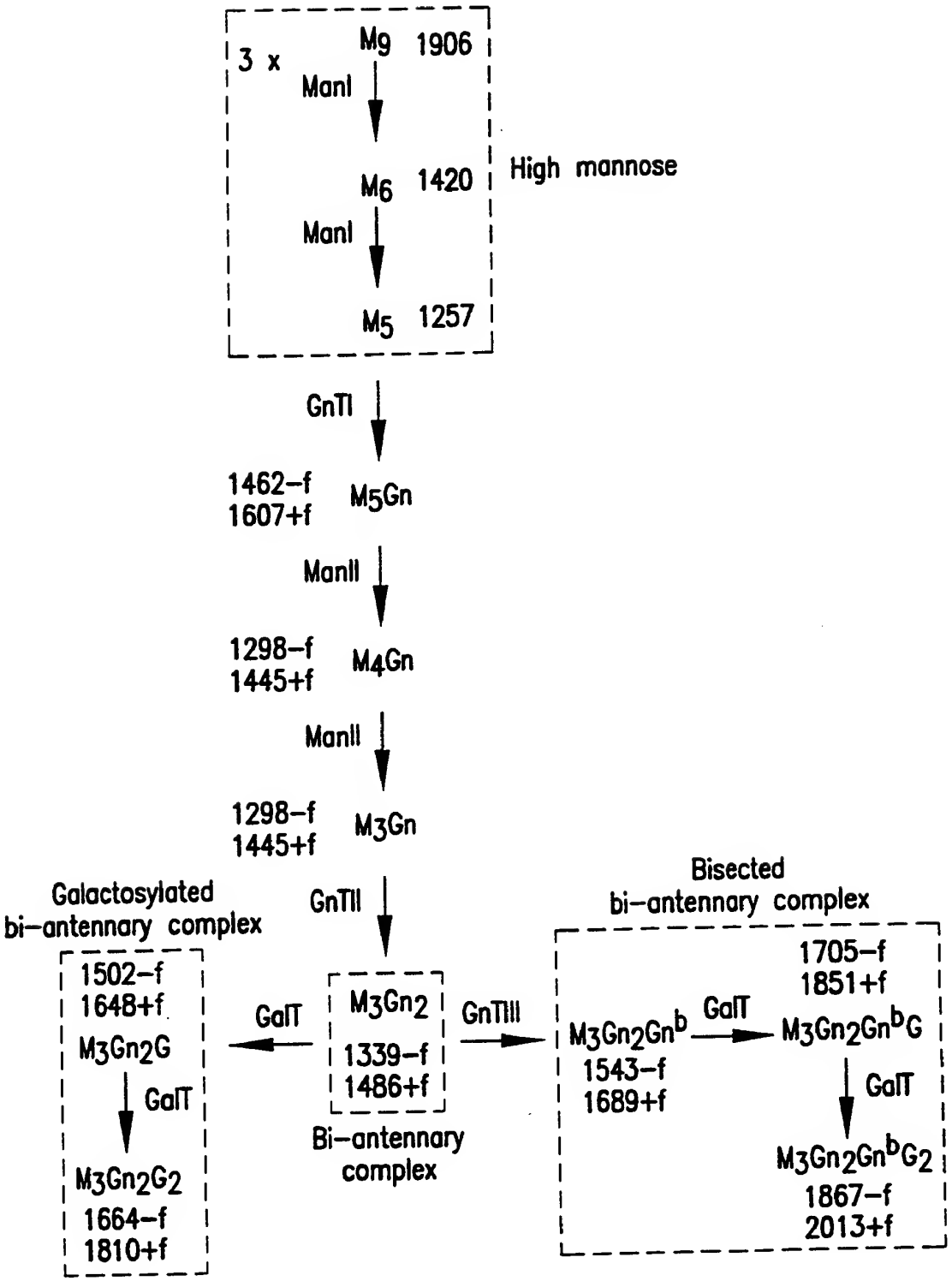

FIG.10

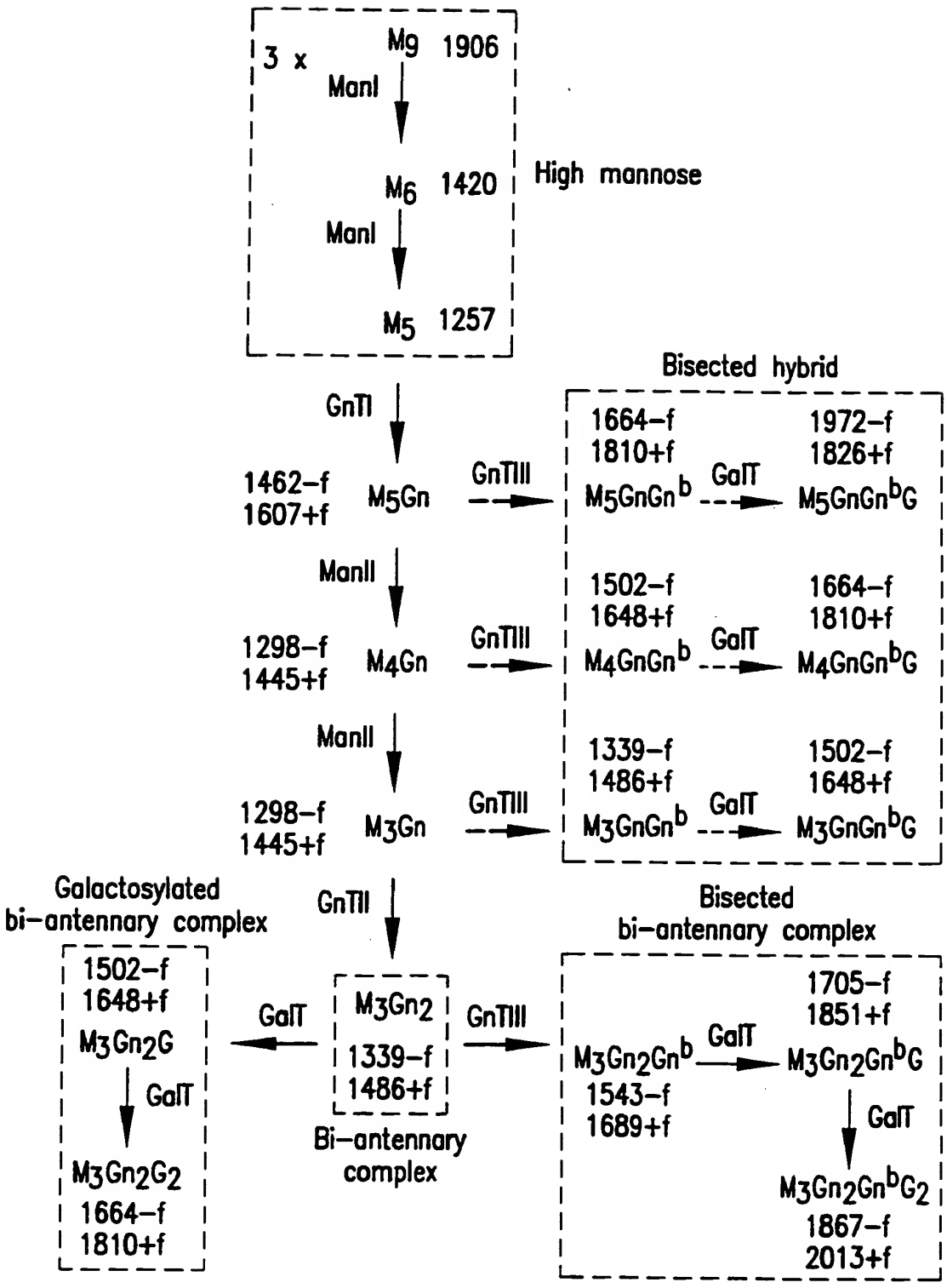

FIG.11

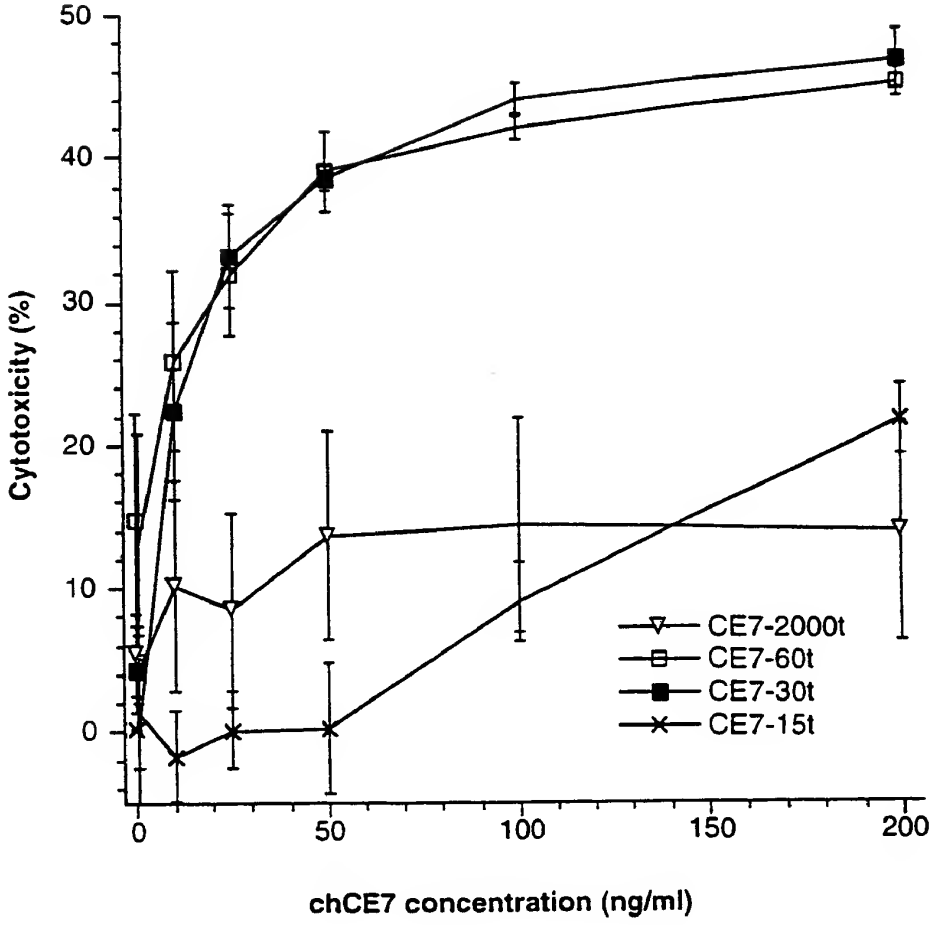

FIG.12

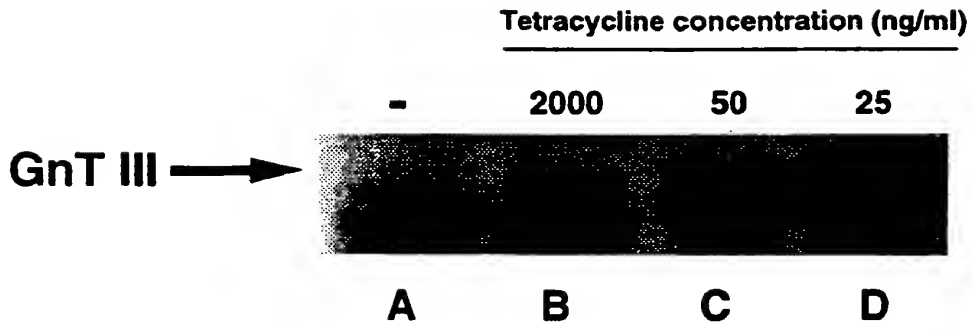

FIG.13

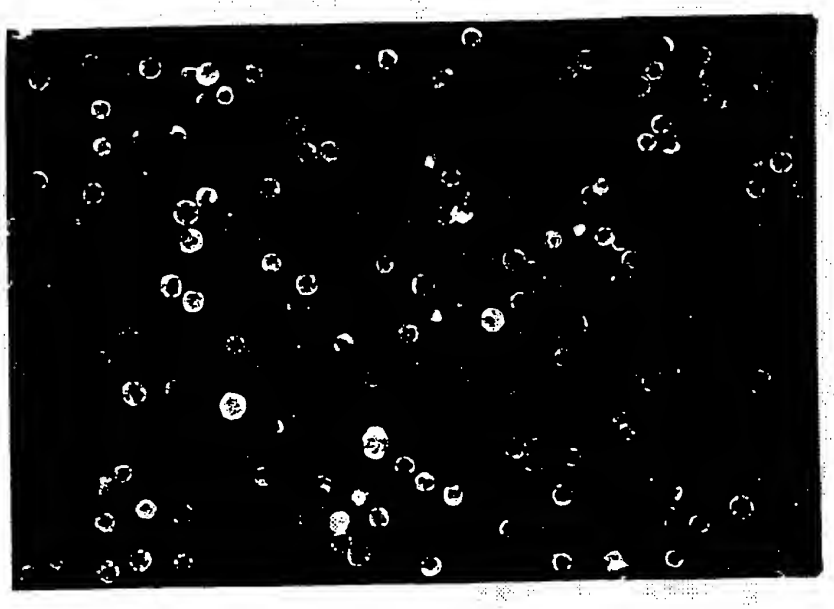

FIG.14A

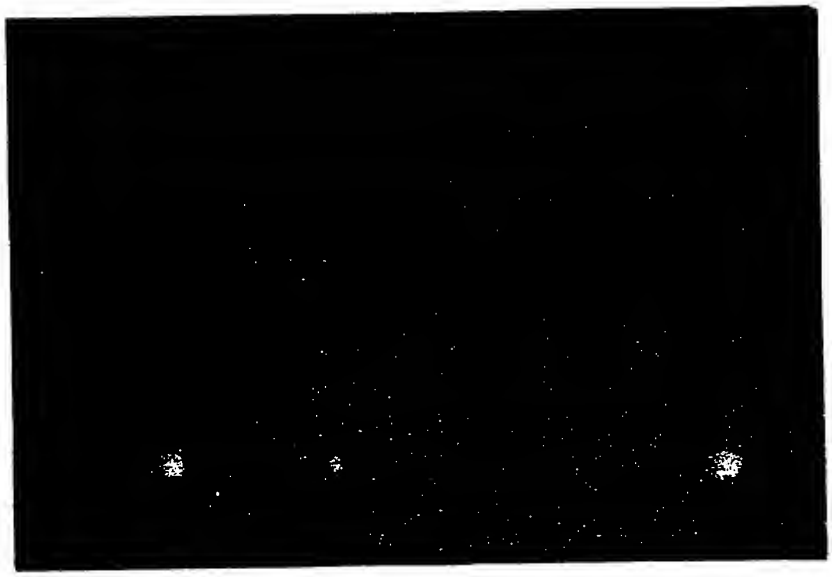

FIG.14B

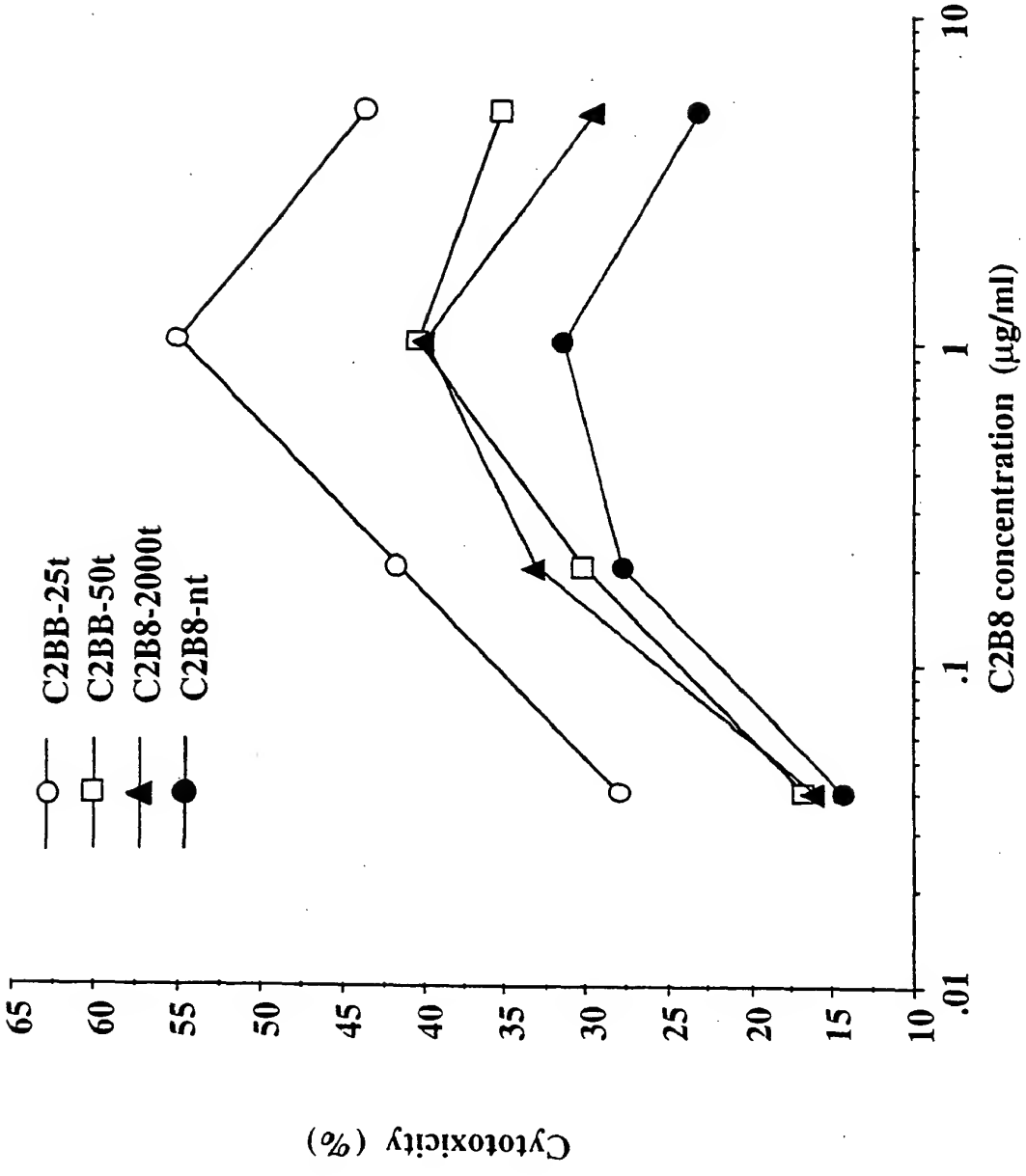

FIG.15

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08711

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/04; A61K 39/395, 38/43; C12N 15/00

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/387.3; 424/133.1, 94.1; 435/328, 69.6, 91.1, 183; 536/23.2, 23.53

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

none

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS. Medline, Biosis

search terms: glycosyl transferase, antibody, immunoglobulin, carbohydrate, N-linked, CHO

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	UMANA et al. Engineered glycoforms of an antineuroblastoma IgG1 with optimized antibody-dependent cellular cytotoxic activity. Nature Biotechnology. February 1999, Vol. 17, pages 176-180, see entire document.	1-85
Y	WRIGHT et al. Effect of glycosylation on antibody function: implications for genetic engineering. Tibtech. 1997, Vol. 15, pages 26-32, see entire document.	1-85
Y	TRILL et al. Production of monoclonal antibodies in COS and CHO cells. Current Opinion in Biotechnology. 1995, Vol. 6, pages 553-555 and 558-560, see entire document.	4, 11-12, 19, 24, 32-35, 38, 63

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 13 JULY 1999	Date of mailing of the international search report 17 AUG 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer JULIE BURKE JOYCE BRIDGERS PARALEGAL SPECIALIST CHEMICAL MATRIX Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08711

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	SBURLATI et al. Synthesis of Bisected glycoforms of recombinant IFN-β by overexpression of β-1,4-N-acetylglucosaminyltransferase III in Chinese Hamster Ovary cells. Biotechnology Progress. 16 April 1998, Vol. 14, pages 189-192, see entire document.	1-6, 8-10 --- 7, 11-85
X --- Y	SBURLATI et al. 'Novel glycoform of recombinant human IFN-beta by overexpression of N-acetyl glucosaminyltransferase III'. Glycoconjugate Journal. 1997, Vol. 14, No. 6, page 781. See Abstract P60.	1-6, 8-10 --- 7, 11-85
Y	AMSTUTZ et al. Production and characterization of a mouse/human chimeric antibody directed against human neuroblastoma. Int. J. Cancer. 1993, Vol. 53, pages 147-152, see entire document.	37, 76
Y	DURR et al. 'First Clinical results with the chimeric antibody chCE7 in neuroblastoma- targeting features and biodistribution data'. Eur J Nucl Med. 12 October 1993, Vol. 20, page 858, see Abstract 159.	37, 76

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/08711

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

530/387.3; 424/133.1, 94.1; 435/328, 69.6, 91.1, 183; 536/23.2, 23.53

Form PCT/ISA/210 (extra sheet)(July 1992)*

been encouraging.[24] Additional potential applications include in vivo B-cell depletion before harvesting peripheral-blood or BM stem cells, as well as possible treatment of patients with autoimmune diseases caused by autoreactive antibodies.

In summary, the IDEC-C2B8 anti-CD20 antibody offers safe, nonmyelosuppressive, well-tolerated therapy with significant activity in patients with relapsed, low-grade B-cell lymphoma.

ACKNOWLEDGMENT

We thank the nurses and staff in the hospitals and clinics a Stanford, Scripps Memorial, and Sydney Kimmel Cancer Center fo their excellent patient care during antibody infusions.

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21 days. Platelets do not express the CD20 antigen or react with IDEC-C2B8, but their Fc receptors can bind to immune complexes, which leads to platelet activation and perhaps removal. This "innocent bystander" effect may account for transient thrombocytopenia following only the first infusion when a large number of circulating B cells were present in the peripheral blood. Since this antibody does not appear to impair marrow reserves, it could possibly be used in patients who are myelosuppressed due to recent chemotherapy or following high-dose chemotherapy with ABMT or peripheral stem-cell rescue. Some alterations in IG levels were noted, but did not result in an increased incidence of infections.

The described AE pattern differs from that found with chemotherapy, radiotherapy, or with other antibodies such as the CAMPATH antibodies, where both incidence and severity of AEs increase with each successive treatment. Most patients in this trial experienced minimal side effects and two patients experienced no AEs.

A pharmacokinetic analysis of IDEC-C2B8 serum levels showed that the C_{max} for both the first and fourth infusions increased with increasing dose. In addition, the C_{max} and serum half-life increased between the first and fourth infusions for most patients. It is known that a majority of normal and malignant circulating B cells are cleared after the first infusion, which has a pronounced effect on the half-life of the antibody. In addition, circulating free antibody is cleared from the serum by antigen present on lymphoma cells. The saturation of these antigenic sites by IDEC-C2B8 during the early portion of the treatment course could also contribute to the differences in the pharmacokinetic profile of the antibody between the first and fourth infusions.

Responses were observed in a variety of clinical situations. Three of 13 patients with extranodal disease had a PR. Responses occurred in patients heavily pretreated with chemotherapy, including aggressive regimens and ABMT, and in patients with bulky disease. Responding sites included BM, lymph nodes, extranodal masses, and spleen.

The antibody appears most active in patients with low-grade or follicular histologies, although the number of patients with aggressive histologies was limited. In the previously published single-dose trial, one PR was documented at each of the 100- and 500-mg/m^2 levels.[20] During this multiple-dose phase I trial, confirmed PRs occurred at all three dose levels: one at 125 mg/m^2, two at 250 mg/m^2, and three at 375 mg/m^2. Response rates were as follows: (1) overall response rate, 30% (six of 20); (2) response rate in assessable patients, 33% (six of 18); and (3) response rate in assessable, low-grade or follicular patients, 37.5% (six of 16). The 375-mg/m^2 dose has been selected for phase II clinical trial evaluation to determine the response rate in patients with follicular or low-grade, relapsed B-cell lymphoma.

Several mechanisms may account for the clinical antitumor activity of this mAb. The construction of a chimeric antibody that contains the human IgG1 heavy-chain constant region greatly augments its capacity to lyse CD20$^+$ B-cell lymphoma targets in vitro using human complement and human effector cells capable of ADCC.[18] In addition, studies have demonstrated that anti-CD20 antibodies may have direct antiproliferative activity on B-lymphoma cell lines, including in some cases the induction of apoptosis.[19,22] However, it is also clear that not all CD20$^+$ cell lines are sensitive to this direct growth inhibition. The CD20 molecule appears to function as a calcium channel and to be involved with progression through the cell cycle.[11] Antibodies that bind to CD20 have been shown to induce cellular protein phosphorylation.[23] Unfortunately, it has been difficult to grow low-grade B-cell lymphoma cells directly from the patient and, thus, it is not known to what extent direct antiproliferative signals mediated through CD20 may contribute to observed clinical activity. Studies to explore these issues are underway in several laboratories.

Multiple therapeutic treatment alternatives are available to patients with relapsed low-grade or follicular lymphoma and range from observation to chemotherapy with single-agent or high-dose protocols that require stem-cell support. In general, a continuous pattern of relapse with mounting cumulative BM toxicity has been observed with these approaches. IDEC-C2B8 represents a novel form of therapy with a unique, minimal toxicity profile. Using the schedule described in this study, the antibody is infused during a brief outpatient treatment and therapy is completed in 22 days. The lack of measurable antiglobulin immune responses makes re-treatment possible. Finally, the lack of substantial short- or long-term toxicity suggests that use of this antibody will not preclude subsequent use of traditional chemotherapy. Potentially, the agent could be used singly, in combination with standard chemotherapy, or following standard chemotherapy in an attempt to decrease minimal residual lymphoma and extend the duration of remission. Preliminary results to explore the combination of this antibody with cyclophosphamide, doxorubicin, vincristine, and prednisone (CHOP) chem therapy have

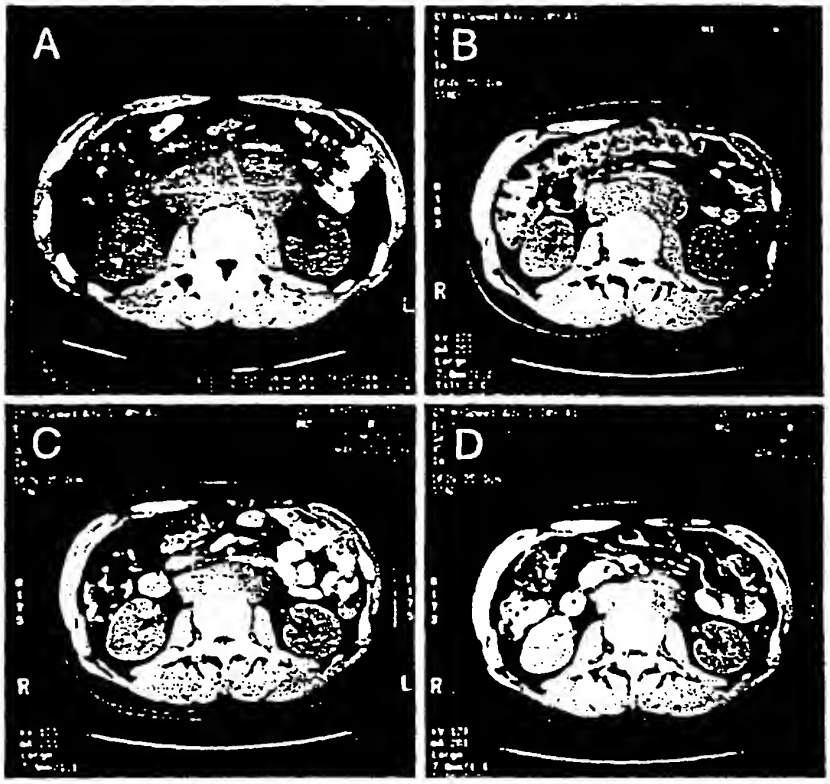

Fig 1. Response to antibody therapy. Images of abdominal mass of patient no. 017 who had progressed following ABMT. (A) Pre-antibody infusion, (B) One month, (C) 3 months, and (D) 6 months posttreatment with 4 infusions of 375 mg/m² IDEC-C2B8 chimeric anti-CD20 mAb.

not identified in the highest dose group and a maximum-tolerated dose (MTD) was not reached. No HAMA responses were identified and one detectable, but not quantifiable, HACA response noted 7 months posttreatment produced no clinical or laboratory abnormalities. Although some infusions were slowed or stopped temporarily, all infusions initiated were completed.

All AEs were reversible and all but one was infusion-related. AEs, classified as primarily grade 1 or 2, were limited to the length of infusion or shortly thereafter. Incidence was highest with the first infusion that coincided with rapid and specific B-cell depletion and subsequent infusions resulted in markedly fewer events. Similar types of AEs have occurred with administration of other biologic agents such as IV gamma globulin. These symptoms seen with the initial infusion may represent biologic effects that result from B-cell depletion. Although the in vivo mechanism of B-cell depletion is unknown, B cells coated in vitro with IDEC-C2B8 are lysed through complement-mediated cytolysis and ADCC using human complement or effector cells.[18] Antibody-coated cell may be removed via Fc-receptor binding and phagocytc sis by the reticuloendothelial system. B-cell lysis or binc ing of immune complexes to Fc receptors on phagocyti cells may lead to cell activation and release of mediator cytokines that could produce the observed infusion-r lated symptoms. The paucity of AEs observed in the se ond through fourth infusions may be explained partial by the depletion of circulating B cells following the fi infusion and by the persistence and accumulation of circ lating antibody observed following the first infusio Other possibilities include tachyphylaxis to secreted cyt kines.

Importantly, only limited myelosuppression with fe significant hematologic changes was observed. Thromb cytopenia, the only AE that lasted significantly beyo the infusion time, occurred in three patients (one of whc had significant thrombocytopenia previously and all whom had marrow involvement pretreatment). Plate levels recovered to greater than 100,000/μL in 3, 7, a

Table 5. Pharmacokinetic Parameter Summary: 375-mg/m² Dose

Patient No.	Model*	First Infusion $T_{1/2}$ (hours)	First Infusion C_{max}† (μg/mL)	First Infusion Cl‡ (L/h)	Fourth Infusion $T_{1/2}$ (hours)	Fourth Infusion C_{max}† (μg/mL)	Fourth Infusion Cl‡ (L/h)	Clinical Response
014	1	35.4	413.7	0.0196	106.0	663.9	0.0045	PD
016§	1	11.1	118.9	0.2820	26.4	131.3	0.1188	PD
017	1	53.1	230.9	0.0441	97.5	504.8	0.0114	PR
Mean		33.2	254.5	0.1152	76.6	433.3	0.0449	
SD		21.1	148.8	0.1449	43.7	273.4	0.0641	

NOTE. Data from the first and fourth infusions analyzed independently.

Abbreviation: $T_{1/2}$, half-life.

*One- or 2-compartment IV infusion model.

†C_{max} is the maximum observed concentration of IDEC-C2B8 attained during the sampling period.

‡Clearance for the first and fourth infusion was determined over comparable time intervals using the equation clearance (Cl) = dose/area under the concentration-time curve.

§The immediate post-fourth infusion sample for patient no. 016 was not available for analysis.

interval, 11% to 55%); PRs were noted in six of 18 patients (one at 125, two at 250, and three at 375 mg/m²). The median time to onset of response for the these six patients was 35.5 days (range, 7 to 64) and the median time to disease progression was 6.4 months (range, 3 to 21.7). MRs were observed in five patients, and seven patients had PD. The mean reduction in measured lesions was 79% (range, 50% to 100%) in responders. At baseline, 13 of 18 assessable patients (72%) had extranodal disease, and three of these 13 had a PR (23%; 50% of responders). Two of 10 patients (20%) with baseline BM invasion responded with a PR. Six of 15 patients (40%) with low-grade histology responded with a PR. Four patients who had undergone prior high-dose therapy with ABMT had the following responses: one PR that lasted 21 months, one MR (30% shrinkage) that lasted 2.6 months, one PD, and one nonassessable patient. Of six patients with bulky disease, four responded with a PR and two had PD.

An example of the clinical response (patient no. 017) following four infusions of 375 mg/m² IDEC-C2B8 is shown in Fig 1. This patient had follicular mixed small- and large-cell (FML) NHL previously treated with aggressive chemotherapy. Relapsed disease was treated with high-dose chemotherapy and total-body irradiation with autologous bone marrow support. PD was noted less than 1 year following high-dose therapy and was treated with chemotherapy. The disease again progressed rapidly and the patient was treated with IDEC-C2B8. Pretreatment computed tomographic images (Fig 1A) dem nstrated a large abdominal mass. Following the fourth mAb infusion, all peripheral disease resolved and the abdominal mass progressively decreased in size as shown on the 3-, 6-, and 9-month images (Fig 1B, C, and D, respectively). The patient remained in PR for 22 months and then had disease progression at a distant site. Biopsy confirmed continued FML histology expressing CD20 and the patient was re-treated at the same dose level and has had an additional ongoing response.

Table 6. Dose-Response Relationship (N = 18)

Response	Dose Group (mg/m²) 125	250	375
CR	0	0	0
PR	1	2	3
SD	1	2	3
PD	1	2	3
OR	1/3 (33%)	2/6 (33%)	3/9 (33%)

NOTE. Two patients were not assessable. Time to progression for PR: 125 dose, 3 months; 250 dose, 6.2+ months to 21 months; 375 dose, 21.7, 4.4, and 10.1 months.

Abbreviations: OR, overall response; SD, stable disease (neither PR/CR or PD).

Three patients had previously received a single infusion of IDEC-C2B8 (50, 100, and 500 mg/m² with no response, mixed response and MR, respectively) in an earlier trial.[20] Upon disease progression, these patients continued to express the CD20 antigen on tumor biopsy with intensity similar to baseline. In the current trial, two responded with a PR and the other was not assessable. Two patients with intermediate-grade bulky disease died 2 and 4 months following treatment due to progressive lymphoma.

DISCUSSION

IDEC-C2B8 is a practical outpatient treatment given over a brief, 3-week course. Dose-limiting toxicities were

ment. Five patients (one each at the lower dose levels and three at 375 mg/m^2) showed hemoglobin reductions (> 1.5 g/dL) and/or hematocrit reduction (> 5%). Platelet counts less than 100,000/μL occurred in three patients (375 mg/m^2) between days 1 and 8; counts recovered within 1 week in two patients and within 3 weeks in the other. The mean WBC count decreased to 2,200/μL in one patient (375 mg/m^2) and recovered within 9 days. Two patients with absolute granulocyte count nadirs less than 1,500/μL (1,200 and 500/μL, respectively) recovered within 1 week. One of these (no. 006), who had a circulating malignant lymphocyte clone of 50,000 to 70,000 μL, had a reduction in absolute granulocyte count to 500/μL on day 1 but recovered on day 8.

Effects on Peripheral-Blood Lymphocyte Subsets

Baseline CD20$^+$ cell counts were high in some patients due to the presence of circulating lymphoma cells. At baseline, two of 17 patients tested had CD20$^+$ monoclonal B-cell populations in peripheral blood and evidence of monoclonality was noted in BM from three of seven patients tested. The CD19$^+$ B-cell population decreased sharply from baseline by day 4 and remained below the lower limits of normal until 6 months posttreatment, at which time recovery began and continued thereafter. The mean percentages of CD3$^+$, CD4$^+$, and CD8$^+$ T cells did not vary significantly from baseline for all patients across all dosing groups.

Effects on Serum Igs and Complement

Mean serum Ig levels remained stable; however, individual patients experienced transient decreases in serum levels of unclear significance. The number of patients with a $\geq$ 20% decline from baseline and with absolute values below the normal range was two, three, and three for IgG, IgA, and IgM, respectively. One patient had decreases in IgG and IgA. Decreases were observed at a median of day 15 with recovery to baseline by study day 22 in five of seven patients. Mean serum complement levels fluctuated and reductions were noted in individual patients; however, no correlation with clinical response or toxicity was evident.

Table 4. Patients With Clinically Significant Hematologic Nadirs

Patient No.	Dosing Group (mg/m^2)	Marrow Involved	Clinically Significant Nadir				
			Hgb	Hct	Platelet	WBC	AGC
002	125	–	×	×			
006	250	+					×
008	250	+	×	×			
012	375	–	×	×		×	×
013	375	+			×		
014	375	–		×			
015	375	+	×	×	×		
016	375	+			×		

NOTE. Clinically significant defined as decrease in hemoglobin (in Hgb) > 1.5 g/dL; decrease in hematocrit (Hct) $\geq$ 5%; WBC count < 3,000/μL; absolute granulocyte count (AGC) < 1,500/μL; platelets < 100,000/μL.

Antibody Serum Pharmacokinetics

Serum levels of free antibody were measured by ELISA. Patients treated at all three dose levels exhibited detectable IDEC-C2B8 serum levels throughout the treatment period. Most patients analyzed showed an accumulation of antibody through the fourth infusion (Table 5). The maximum concentration (C_{max}) and serum half-life of IDEC-C2B8 increased between the first and fourth infusions for most patients, most likely due to the clearance of circulating B cells from the peripheral blood and saturation of CD20-binding sites after the first infusion. At the 375-mg/m^2 dose, the mean serum half-life after the first infusion was 33.2 hours (range, 11.1 to 53.1), while the mean serum half-life after the fourth infusion was 76.6 hours (range, 26.4 to 106.0). Wide interpatient variability was noted, both within and between dose groups, likely due to variable amounts of circulating tumor, overall tumor burden, and available CD20 antigen. No correlation was noted between any of the pharmacokinetic parameters and response to treatment.

Laboratory and Immune Response Tests

No clinically significant alterations in urinalysis, or in mean values for serum albumin, LDH, AST, ALT, uric acid, bilirubin, alkaline phosphatase, or creatinine were noted. No evidence of acute tumor lysis syndrome was noted using Hande's method.[21] No quantifiable HAMA immune response was noted, although one patient experienced a detectable but not quantifiable HACA response 7 months posttreatment that did not result in any clinical or laboratory abnormality.

Overall Clinical Response

Two patients were not assessable for efficacy; treatment was discontinued after one dose due to grade 4 thrombocytopenia in one and elevated liver enzymes later attributed to malignant lymphoma in the other. The 18 assessable patients were staged at baseline and restaged 1 and 3 months after treatment completion. Responders were reevaluated every 3 months until disease progression. Responses are listed in Table 6.

The overall response rate was 33% (95% confidence

Table 3. Incidence of Most Frequent AEs by Dosing Group, Event, and Patient (N = 20)

Variable	Dosing Group (mg/m²) 125 No. of Patients	125 No. of Events	250 No. of Patients	250 No. of Events	375 No. of Patients	375 No. of Events	Total (N = 20) No. of Patients	Total (N = 20) %	Total (N = 20) No. of Events	Total (N = 20) %
Any AE	3	19	7	34	9	59	19	95.0	112	100.0
Body as a whole										
Fever	3	4	6	10	8	19	17	85.0	33	29.5
Chills	2	2	5	7	2	2	9	45.0	11	9.8
Asthenia	1	1	4	4	4	4	9	45.0	9	8.0
Night sweats	1	1	0	0	2	2	3	15.0	3	2.7
Digestive system										
Nausea	2	2	1	1	2	2	5	25.0	5	4.5
Vomiting	1	1	1	1	2	2	4	20.0	4	3.6
Dyspepsia	0	0	1	2	1	1	2	10.0	3	2.7
Blood or BM										
Thrombocytopenia	0	0	0	0	3	3	3	15.0	3	2.7
Coagulation disorder	0	0	0	0	2	2	2	10.0	2	1.8
Musculoskeletal system										
Arthralgia	0	0	1	1	1	1	2	10.0	2	1.8
Nervous system										
Vasodilation	0	0	0	0	1	3	1	5.0	3	2.7
Respiratory system										
Rhinitis	0	0	0	0	2	2	2	10.0	2	1.8
Skin and appendages										
Pruritus	0	0	1	1	1	2	2	10.0	3	2.7
Rash	0	0	0	0	2	2	2	10.0	2	1.8
Urticaria	1	1	0	0	1	2	2	10.0	3	2.7

NOTE. AEs probably or possibly related or of unknown relationship to treatment with frequency ≥ 1% of events.

112 were reported as related to study treatment (66%) and are listed in Table 3. AEs were most frequently infusion-related and resolved completely, usually within hours. Hematologic toxicity and infections were seen in a minority of patients and were usually mild. No clinically significant renal or hepatic toxicity was observed. No apparent relationship was noted between dose and severity of AEs. AEs occurred primarily at the first infusion and the number of AEs decreased dramatically during subsequent infusions. The most frequent infusion-related events were fever, asthenia, chills, nausea, vomiting, rash, and urticaria. Grade 2 hypotension, reported in one patient, resolved with treatment and did not require hospitalization. Non–infusion-related toxicities occurred in a minority of patients. Although most (91%) AEs were classified as grades 1 or 2, nine events that occurred in six patients were noted as severe (grade 3 or 4). Eight grade 3 events consisted of pain (two episodes), thrombocytopenia (two), fatigue, rigors, nausea, and bronchospasm (one each). Grade 4–related thrombocytopenia occurred within 24 hours of the first infusion in one patient (no. 015) with small lymphocytic histology and extensive BM involvement. This patient had previously experienced grade 3 thrombocytopenia with a single infusion of IDEC-C2B8. The platelet count declined from a baseline value of 93,000/μL to a nadir of 19,000/μL, lactate dehydrogenase (LDH) increased markedly from a baseline of 629 U/L to a peak of 2,660 U/L, and hemoglobin decreased from 12.6 g/dL to 7.8 g/dL. Uric acid peaked to 10.5 mg/dL within 24 to 48 hours. The patient was treated with fluids, allopurinol, corticosteroids, and a single platelet transfusion. Evaluation for disseminated intravascular coagulation was nondiagnostic, and the patient improved with normalization of LDH, platelet count, and hemoglobin level by day 31. This patient did not require hospitalization and received no further IDEC-C2B8 treatment.

Effects on Hematologic Parameters

Hematologic toxicity was usually mild and reversible and is listed in Table 4. The median nadirs calculated for WBC, granulocytes, hemoglobin, and hematocrit did not substantially deviate from baseline and did not change over dose groups. Three patients with trilineage hematologic effects recovered in ≤ 7 days, ≤ 19 days, and ≤ 35 days, respectively. Five of eight patients (63%) with clinically significant hematologic nadirs had BM involv -

Table 1. Patient Characteristics

Characteristic	Dosing Group (mg/m²) 125 (n = 3)	250 (n = 7)	375 (n = 10)	Total (N = 20) No.	%
Age (years)					
Median	48.0	59.0	59.5	59.0	
Range	41-70	33-72	29-81	29-81	
Sex					
Female	1	3	6	10	50
Male	2	4	4	10	50
Race					
White	3	6	9	18	90
Asian	0	1	1	2	10
Histologic grade*					
Low	2	5	8	15	75
A	0	0	1	1	5
B	0	3	5	8	40
C	2	2	2	6	30
Intermediate	0	2	2	4	20
D	0	0	1	1	5
E	0	1	0	1	5
G	0	1	1	2	10
High	1	0	0	1	5
H	1	0	0	1	5
Stage†					
I	0	0	2	2	10
II	0	1	0	1	5
III	2	1	4	7	35
IV	1	5	4	10	50

*Based on the International Working Formulation.
†Stage at initial diagnosis, based on the stage grouping.

Table 2. Summary of Prior Therapy (N = 20)

Type of Prior Therapy	Prior Therapies No.	Median	Range	Time From Last Therapy (months) Median	Range
Chemotherapy	20	2	1-4	6.6	0.9-67.
Bioimmunotherapy	4	1	1-2	6.5	4.4-24.
Radiotherapy	8	1	1-2	30.1	5.0-10
ABMT	4	1	1-1	13.5	5.0-31.
All therapy	20	3	1-6	5.3	0.9-10

*Months to first IDEC-C2B8 infusion from stop date of last therapy.

Sample Size

A minimum of three patients and a maximum of nine assessable patients were entered at each dose level. Dose- and drug-related toxicity determinations were the primary study objectives, and no statistical analyses were performed.

Assessability Criteria and Concurrent Treatment Conditions

All patients who received one or more IDEC-C2B8 doses were considered assessable for safety. Patients were assessable for efficacy if they completed one full course of treatment (four doses), satisfied all prestudy criteria, had measurable disease, and met criteria for evaluation of response. No concomitant cancer chemotherapy, radiotherapy, hormonal therapy, or immunotherapy was allowed.

RESULTS

Demographics

Twenty patients received weekly IV infusions times four of IDEC-C2B8. Patient characteristics and prior lymphoma therapies are listed in Tables 1 and 2. Three patients (median age, 48.0 years) received 125 mg/m², seven patients (median age, 59.0 years) 250 mg/m², and 10 patients (median age, 59.5 years) 375 mg/m². T original diagnosis was low-grade NHL in 15 patie (75%) and intermediate- or high-grade disease in fi (25%). Advanced-stage (III/IV) lymphoma was prese at diagnosis in 17 patients. All patients required thera due to disease progression and had failed to respond prior chemotherapy (median of 2.0 prior regimens; Tal 2). The median duration of response to last chemothera before IDEC-C2B8 treatment was 5.0 months. At ba line, three patients had lesions with measurements ≥ cm and three had lesions that measured ≥ 10 cm. Marr involvement was present in 50% of patients and 13 of (65%) had extranodal disease. All patients, includi those previously exposed to murine antibodies, were n ative for HAMA. Four patients had progressed followi autologous bone marrow transplantation (ABMT) a three patients had received a single infusion of IDE C2B8 in an earlier phase 1 single-dose trial.[20]

Infusion Data

Patients were treated primarily on an outpatient ba Routine premedication was not given; however, patie received oral diphenhydramine and acetaminophen wl appropriate. If the infusion was stopped due to signific infusion-related adverse events (AEs), it was restar within 30 to 45 minutes at a lower rate (50 to 100 r h) and increased as tolerated to 200 mg/h. The m infusion time across all infusions was 3.6, 3.8, and hours in the 125-, 250-, and 375-mg/m² treatment grou respectively. The overall mean infusion time was hours (range, 2.5 to 7.1 hours). The mean total dose ministered over the course of four infusions was appr mately 947, 1,715, and 2,535 mg in the 125-, 250-, 375-mg/m² treatment groups, respectively. The maxim total dose administered was 3,200 mg in two patient the 375-mg/m² treatment group.

Infusion-Related Toxicity

Eighteen patients received all four weekly infusio two patients received only one infusion. Of 169 total A

CD20 antigen, induces CDC and ADCC of antigen-positive cells,[18] induces apoptosis of some lymphoma cell lines, and increases sensitivity to the cytotoxic effect of chemotherapy/toxins in some resistant human lymphoma cell lines.[19] Preclinical data in cynomolgus monkeys showed B-lymphocyte depletion in peripheral blood, bone marrow (BM), and lymph nodes without dose-limiting toxicity.[18]

Clinical data from a phase 1, single dose-escalating (10 to 500 mg/m^2) study in 15 patients with relapsed NHL demonstrated no dose-limiting toxicity and showed clinical activity (two PRs and four minor responses [MRs]).[20] Antibody infusion caused CD20$^+$ B-cell depletion in peripheral blood at 24 to 72 hours that persisted for 2 to 3 months in most patients. Flow cytometry evaluation of cell suspensions from lymph node biopsy specimens showed B-cell depletion and tumor cells coated with antibody 2 weeks posttreatment.

Here, we report results from a phase I dose-escalation trial that used multiple infusions of IDEC-C2B8 (125, 250, or 375 mg/m^2) in 20 patients with relapsed B-cell lymphoma. Primary study objectives included evaluation of safety and dose-limiting toxicities, determination of a biologically active tolerated dose (BATD), pharmacokinetic analysis, determination of the degree and duration of B-cell depletion, and analysis of relevant clinical activity.

PATIENTS AND METHODS

Protocol Design

Intravenous (IV) infusions weekly times four of IDEC-C2B8 at doses of 125, 250, or 375 mg/m^2 were given to patients with relapsed B-cell NHL. Evaluation of safety, dose-limiting toxicities, and clinical activity was performed, and circulating levels of IDEC-C2B8, HAMA, and human antichimeric antibody (HACA) levels were analyzed.

Patients

Adults with histologically confirmed, relapsed B-cell lymphoma that expressed the CD20 antigen were eligible. All patients met the following criteria: expected survival duration ≥ 3 months with no serious nonmalignant disease; prestudy performance status of 0, 1, or 2 on the World Health Organization (WHO) scale; negative for human immunodeficiency virus and hepatitis-B surface antigen; and serum IgG level ≥ 600 mg/dL, hemoglobin ≥ 8.0 g/dL, WBC count ≥ 3.0 × 10^3/μL, absolute granulocyte count ≥ 1.5 × 10^3/μL, platelet count ≥ 75 × 10^3/μL, bilirubin level less than 1.5 mg/dL, alkaline phosphatase level less than two times normal, AST less than two times normal, and serum creatinine concentration less than 2.0 mg/dL. All patients tested negative for HAMA. All patients signed an informed consent approved by the institutional review boards of Stanford University Medical Center, Palo Alto, CA, Sydney Kimmel Cancer Center, or Scripps Memorial Hospital, San Diego, CA.

IDEC-C2B8 Serum Analysis

Serum levels of IDEC-C2B8 were measured by enzyme-linked immunosorbent assay (ELISA). Microtiter plates were coated with purified polyclonal goat anti-IDEC-2B8-specific antibody. Patient serum was serially diluted across the plate and bound human IgG detected by goat antihuman IgG conjugated with horseradish peroxidase. Color was developed by adding 3-ethylbenzthiazoline sulfonic acid (ABTS) substrate. Known amounts of IDEC-C2B8 diluted into normal human serum were used to make a standard curve on each plate. Antibody concentration was determined by comparing the signal from the patients' sera to that from the standard curve.

Measurement of Host Anti–IDEC-C2B8 Antibody Response

Posttreatment sera from 1-, 2-, and 3-month evaluations were analyzed for the presence of a host antichimeric antibody immune response using a sandwich ELISA. Microtiter plates were coated with IDEC-C2B8. Dilutions of the patient's sera were added and, following washing, detected with biotin-labeled IDEC-C2B8 followed by avidin horseradish peroxidase (HRP) and the substrate ABTS. The minimum quantifiable level for these assays was 100 ng/mL (detectable to 5 ng/mL).

Flow Cytometry

Flow cytometry of peripheral blood was performed to determine the following lymphocyte subsets: CD3$^+$, CD4$^+$, and CD8$^+$ T cells; CD19$^+$ and CD20$^+$ B cells; and expression of surface Ig light chains. Samples were obtained before and 72 hours after the first infusion, at 1 and 3 months, and then every 3 months for 1 year. When available, tumor cells were obtained from excisional biopsies, fine-needle tumor aspirations, or bone marrow. Tumor-cell expression of CD20 was determined using fluorescein isothiocyanate (FITC)-conjugated mAb by flow cytometry or HRP-labeled L26 (DAKO, Carpinteria, CA) in paraffin-embedded tissue by immunohistochemistry. Tumor cells were analyzed for expression of surface Ig light chains using antihuman kappa- and antihuman lambda-conjugated antibodies.

Study Measurements

Infusion-related toxicity was evaluated using the National Cancer Institute's adult toxicity criteria. Measurements during treatment included analysis of hematologic, renal, and hepatic function; serum complement; and Igs. Tumor response was evaluated 1 and 3 months after treatment completion and every 3 months for a maximum of 1 year using tumor measurements obtained during physical examination and from radiologic imaging studies. The WHO/Eastern Cooperative Oncology Group (ECOG) guidelines for CR (complete resolution of all detectable disease), PR (> 50% reduction in measurable disease persisting for at least 28 days), MR (25% to 50% reduction in disease), and stable disease (no significant change in tumor measurements without progression over the period of observation) were used. Progressive disease (PD) was defined as a 25% increase in measurable disease or the appearance of any new lesion. Time to progression was measured from date of first study treatment to first date when PD was documented. All responses were confirmed through repeat evaluation ≥ 28 days after initial efficacy determination.

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IDEC-C2B8: Results of a Phase I Multiple-Dose Trial in Patients With Relapsed Non-Hodgkin's Lymphoma

By David G. Maloney, Antonio J. Grillo-López, David J. Bodkin, Christine A. White, Tino-Morie Liles, Ivor Royston, Chet Varns, Jay Rosenberg, and Ronald Levy

Purpose: To evaluate the safety, pharmacokinetics, and biologic effect of multiple doses of the chimeric anti-CD20 monoclonal antibody (mAb) IDEC-C2B8 in patients with relapsed B-cell lymphoma.

Patients and Methods: Twenty patients with relapsed low-grade (n = 15) or intermediate-/high-grade (n = 5) lymphoma received weekly infusions times four of 125 mg/m^2 (n = 3), 250 mg/m^2 (n = 7), or 375 mg/m^2 (n = 10) of IDEC-C2B8.

Results: Infusional side effects during the initial infusion were mainly grade I/II fever, asthenia, chills, nausea, rash, and urticaria. More serious events were rare. Peripheral-blood B cells were rapidly depleted and slowly recovered over 3 to 6 months. There was no change in mean immunoglobulin (Ig) levels. Antibody serum half-life (and maximum concentration [C_{max}]) generally increased between the first and fourth infusions (33.2 hours v 76.6 hours, respectively) following the 375-mg/m^2 doses. Six of 18 assessable patients had a partial remission (PR), with a median time to disease progression of 6.4 months (range, 3 to 21.7). Minor responses (MRs) were observed in five patients and progressive disease (PD) in seven. Tumor responses occurred in peripheral blood, bone marrow (BM), spleen, bulky lymph nodes, and extranodal sites, and in patients who had relapsed following high-dose myeloablative chemotherapy. Six of 14 patients (40%) with a low-grade histology responded. Four of six with bulky disease had a PR.

Conclusion: IDEC-C2B8 chimeric anti-CD20 mAb therapy is well tolerated and has clinical activity in patients with relapsed B-cell lymphoma. The 375-mg/m^2 dose has been selected for a phase II trial in patients with relapsed low-grade or follicular B-cell lymphoma.

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THE B-CELL–SPECIFIC CD20 antigen is an attractive target for monoclonal antibody (mAb) immunotherapy of B-cell non-Hodgkin's lymphoma (NHL).[1] More than 90% of B-cell NHLs express the CD20 antigen.[2] The antigen does not internalize,[3] is not shed from the cell surface,[3] and does not circulate as free protein.[4] Antigen expression occurs during the pre–B-cell stage of differentiation and persists through mature B-cell development, but is not expressed on early pre-B cells, stem cells, or antigen-presenting dendritic reticulum cells.[5] While the exact function of CD20 is not known, the antigen may regulate a step in the B-cell activation process required for cell-cycle initiation and differentiation[6-11] and may function as a calcium channel.[12]

Limited experience has been reported using unmodified murine anti-CD20 antibodies. A phase I trial that used the murine immunoglobulin G2a (IgG2a) anti-CD20 antibody 1F5 produced one partial remission (PR) in the treatment of four patients.[3] Radiolabeling murine anti-CD20 mAbs has been more widely evaluated. Treatment with marrow ablative doses of iodine 131–labeled 1F5 or B1[13,14] with autologous marrow rescue induced complete responses (CR) in most patients. In addition, therapy with lower doses of ^{131}I-B1 has demonstrated significant clinical activity,[15,16] including responses to the trace-labeled antibody. Finally, infusion of IDEC-Y2B8, a murine anti-CD20 antibody radiolabeled with yttrium 90 (20 to 5 mCi) resulted in four CRs and five PRs in a phase I study in 14 refractory B-cell lymphoma patients.[17] Autologous stem-cell rescue was required at the highest doses.

Most murine antibodies do not effectively activate human complement-dependent cytotoxicity (CDC) and antibody-dependent cellular cytotoxicity (ADCC) effector mechanisms. In addition, repeated murine antibody infusions may result in the formation of a human antimouse antibody (HAMA) response that limits further clinical use. IDEC-C2B8 is an IgG1 kappa chimeric mAb that consists of variable regions from the heavy and light chains of the murine anti-CD20 antibody (IDEC-2B8) and human IgG1 and kappa constant regions.[18] This augments the lysis of target tumor cells using human CDC or ADCC mechanisms and decreases immunogenicity. High yields of this chimeric antibody are produced in suspension culture by Chinese hamster ovary cells.[18] In vitro, IDEC-C2B8 has specificity and affinity for

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